IPE JUN 18 2004 JC16 PATENT & TRADEMARK OFFICE

SEQUENCE LISTING

```
<110> MA, Jing
      GUO, Yajun

<120> PREPARATION AND APPLICATION OF
      ANTI-TUMOR BIFUNCTIONAL FUSION PROTEINS



<130> 549062000200

<140> US 10/723,003
<141> 2003-11-26

<150> CN 2003101199300
<151> 2003-11-25

<150> CN 031292909
<151> 2003-06-13

<160> 68

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 546
<212> DNA
<213> Homo sapiens

<400> 1
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agctcgggac tcagtgggac ccaggactgc tccttccaac acagccccat ctcctccgac 120
ttcgctgtca aaatccgtga gctgtctgac tacctgcttc aagattaccc agtcaccgtg 180
gcctccaacc tgcaggacga ggagctctgc gggggcctct ggcggctggt cctggcacag 240
cgctggatgg agcggctcaa gactgtcgct gggtccaaga tgcaaggctt gctggagcgc 300
gtgaacacgg agatacactt tgtcaccaaa tgtgcctttc agcccccccc cagctgtctt 360
cgcttcgtcc agaccaacat ctcccgcctc ctgcaggaga cctccgagca gctggtggcg 420
ctgaagccct ggatcactcg ccagaacttc tcccggtgcc tggagctgca gtgtcagccc 480
gactcctcaa ccctgccacc cccatggagt ccccggcccc tggaggccac agccccgaca 540
gccccg                                                            546

<210> 2
<211> 182
<212> PRT
<213> Homo sapiens

<400> 2
Met Thr Val Leu Ala Pro Ala Trp Ser Pro Thr Thr Tyr Leu Leu Leu
 1               5                   10                  15
Leu Leu Leu Leu Ser Ser Gly Leu Ser Gly Thr Gln Asp Cys Ser Phe
             20                  25                  30
Gln His Ser Pro Ile Ser Ser Asp Phe Ala Val Lys Ile Arg Glu Leu
         35                  40                  45
Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val Thr Val Ala Ser Asn Leu
     50                  55                  60
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Gln Asp Glu Glu Leu Cys Gly Gly Leu Trp Arg Leu Val Leu Ala Gln
65                  70                  75                  80
Arg Trp Met Glu Arg Leu Lys Thr Val Ala Gly Ser Lys Met Gln Gly
                85                  90                  95
Leu Leu Glu Arg Val Asn Thr Glu Ile His Phe Val Thr Lys Cys Ala
            100                 105                 110
Phe Gln Pro Pro Pro Ser Cys Leu Arg Phe Val Gln Thr Asn Ile Ser
        115                 120                 125
Arg Leu Leu Gln Glu Thr Ser Glu Gln Leu Val Ala Leu Lys Pro Trp
    130                 135                 140
Ile Thr Arg Gln Asn Phe Ser Arg Cys Leu Glu Leu Gln Cys Gln Pro
145                 150                 155                 160
Asp Ser Ser Thr Leu Pro Pro Pro Trp Ser Pro Arg Pro Leu Glu Ala
                165                 170                 175
Thr Ala Pro Thr Ala Pro
            180
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<210> 3
<211> 1242
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 3

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atgacagtgc tggcgccagc ctggagccca acaacctatc tcctcctgct gctgctgctg 60
agctcgggac tcagtgggac ccaggactgc tccttccaac acagccccat ctcctccgac 120
ttcgctgtca aaatccgtga gctgtctgac tacctgcttc aagattaccc agtcaccgtg 180
gcctccaacc tgcaggacga ggagctctgc gggggcctct ggcggctggt cctggcacag 240
cgctggatgg agcggctcaa gactgtcgct gggtccaaga tgcaaggctt gctggagcgc 300
gtgaacacgg agatacactt tgtcaccaaa tgtgcctttc agcccccccc cagctgtctt 360
cgcttcgtcc agaccaacat ctcccgcctc ctgcaggaga cctccgagca gctggtggcg 420
ctgaagccct ggatcactcg ccagaacttc tcccggtgcc tggagctgca gtgtcagccc 480
gactcctcaa ccctgccacc cccatggagt ccccggcccc tggaggccac agccccgaca 540
gccccggagc ccaaatcttg tgacaaaact cacacatgcc caccgtgccc agcacctgaa 600
ctcctggggg gaccgtcagt cttcctcttc cccccaaaac ccaaggacac cctcatgatc 660
tcccggaccc ctgaggtcac atgcgtggtg gtggacgtga gccacgaaga ccctgaggtc 720
aagttcaact ggtacgtgga cggcgtggag gtgcataatg ccaagacaaa gccgcgggag 780
gagcagtaca acagcacgta ccgggtggtc tgcgtcctca ccgtcctgca ccaggactgg 840
ctgaatggca aggagtacaa gtgcaaggtc tccaacaaag ccctcccagc ccccatcgag 900
aaaaccatct ccaaagccaa agggcagccc cgagaaccac aggtgtacac cctgccccca 960
tcccgggatg agctgaccaa gaaccaggtc agcctgacct gcctggtcaa aggcttctat 1020
cccagcgaca tcgccgtgga gtgggagagc aatgggcagc cggagaacaa ctacaagacc 1080
acgcctcccg tgctggactc cgacggctcc ttcttcctct acagcaagct caccgtggac 1140
aagagcaggt ggcagcaggg gaacgtcttc tcatgctccg tgatgcatga ggctctgcac 1200
aaccactaca cgcagaagag cctctccctg tctccggta aa                    1242
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<210> 4
<211> 414
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

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<400> 4
Met Thr Val Leu Ala Pro Ala Trp Ser Pro Thr Thr Tyr Leu Leu Leu
 1               5                  10                  15
Leu Leu Leu Leu Ser Ser Gly Leu Ser Gly Thr Gln Asp Cys Ser Phe
            20                  25                  30
Gln His Ser Pro Ile Ser Ser Asp Phe Ala Val Lys Ile Arg Glu Leu
        35                  40                  45
Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val Thr Val Ala Ser Asn Leu
    50                  55                  60
Gln Asp Glu Glu Leu Cys Gly Gly Leu Trp Arg Leu Val Leu Ala Gln
65                  70                  75                   80
Arg Trp Met Glu Arg Leu Lys Thr Val Ala Gly Ser Lys Met Gln Gly
                85                  90                  95
Leu Leu Glu Arg Val Asn Thr Glu Ile His Phe Val Thr Lys Cys Ala
            100                 105                 110
Phe Gln Pro Pro Pro Ser Cys Leu Arg Phe Val Gln Thr Asn Ile Ser
        115                 120                 125
Arg Leu Leu Gln Glu Thr Ser Glu Gln Leu Val Ala Leu Lys Pro Trp
    130                 135                 140
Ile Thr Arg Gln Asn Phe Ser Arg Cys Leu Glu Leu Gln Cys Gln Pro
145                 150                 155                 160
Asp Ser Ser Thr Leu Pro Pro Pro Trp Ser Pro Arg Pro Leu Glu Ala
                165                 170                 175
Thr Ala Pro Thr Ala Pro Glu Pro Lys Ser Cys Asp Lys Thr His Thr
            180                 185                 190
Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe
        195                 200                 205
Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
    210                 215                 220
Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
225                 230                 235                 240
Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
                245                 250                 255
Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
            260                 265                 270
Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
        275                 280                 285
Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
    290                 295                 300
Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
305                 310                 315                 320
Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
                325                 330                 335
Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
            340                 345                 350
Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
        355                 360                 365
Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
    370                 375                 380
Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
385                 390                 395                 400
Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
                405                 410


<210> 5
<211> 45
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<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 5
ggcggtggag gctctggtgg aggcggttca ggaggcggtg gatct 45

<210> 6
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 6
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1 5 10 15

<210> 7
<211> 426
<212> DNA
<213> Mus musculus

<400> 7
atcgccgcca ccatggaatg gagttggata tttctctttc tcctgtcagg aactgcaggt 60
gtccactctg aggtccagct gcagcagtct ggacctgagc tggtaaagcc tggggcttca 120
gtgaagatgt cctgcaaggc ttctggatac acattcacta gctatgttat gcactgggtg 180
aagcagaagc ctgggcaggg ccttgactgg attggatata ttgttcctta caatgatggc 240
actaagtaca atgagaagtt caaaggcaag gccacactga cttcagacaa atcctccagc 300
acagcctaca tggagctcag cagactgacc tctgaggact ctgcggtcta ttattgtgtc 360
tacggtagta ggtacgactg gtatttagat gtctggggcg cagggaccac ggtcaccgtc 420
tcctca 426

<210> 8
<211> 138
<212> PRT
<213> Mus musculus

<400> 8
Met Glu Trp Ser Trp Ile Phe Leu Phe Leu Leu Ser Gly Thr Ala Gly
1 5 10 15
Val His Ser Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys
20 25 30
Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe
35 40 45
Thr Ser Tyr Val Met His Trp Val Lys Gln Lys Pro Gly Gln Gly Leu
50 55 60
Asp Trp Ile Gly Tyr Ile Val Pro Tyr Asn Asp Gly Thr Lys Tyr Asn
65 70 75 80
Glu Lys Phe Lys Gly Lys Ala Thr Leu Thr Ser Asp Lys Ser Ser Ser
85 90 95
Thr Ala Tyr Met Glu Leu Ser Arg Leu Thr Ser Glu Asp Ser Ala Val
100 105 110

```
Tyr Tyr Cys Val Tyr Gly Ser Arg Tyr Asp Trp Tyr Leu Asp Val Trp
        115                 120                 125
Gly Ala Gly Thr Thr Val Thr Val Ser Ser
    130                 135


<210> 9
<211> 465
<212> DNA
<213> Mus musculus

<400> 9
atcatcacca gaacagctta cgagcagacc gccagacagc tcacagggat caagcttgcc 60
gccaccatgg aatcacagac tcaggtcttc ctctccctgc tgctctgggt atctggtacc 120
tgtgggaaca ttatgatgac acagtcgcca tcatctctgg ctgtgtctgc aggagaaaag 180
gtcactatga gctgtaagtc cagtcaaagt gttttataca gttcaaatca gaagaactac 240
ttggcctggt accagcagaa accagggcag tctcctaaac tgctgatcta ctgggcatcc 300
actagggaat ctggtgtccc tgatcgcttc acaggcagtg gatctgggac agattttact 360
cttaccatca gcagtgtaca agctgaagac ctggcagttt attactgtca tcaatatttc 420
tcctcataca cgttcggagg ggggaccaag ctggaaataa agcgg                 465

<210> 10
<211> 133
<212> PRT
<213> Mus musculus

<400> 10
Met Glu Ser Gln Thr Gln Val Phe Leu Ser Leu Leu Leu Trp Val Ser
 1               5                  10                  15
Gly Thr Cys Gly Asn Ile Met Met Thr Gln Ser Pro Ser Ser Leu Ala
            20                  25                  30
Val Ser Ala Gly Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser
        35                  40                  45
Val Leu Tyr Ser Ser Asn Gln Lys Asn Tyr Leu Ala Trp Tyr Gln Gln
    50                  55                  60
Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg
65                  70                  75                  80
Glu Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp
                85                  90                  95
Phe Thr Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Val Tyr
            100                 105                 110
Tyr Cys His Gln Tyr Phe Ser Ser Tyr Thr Phe Gly Gly Gly Thr Lys
        115                 120                 125
Leu Glu Ile Lys Arg
    130


<210> 11
<211> 2021
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 11
atcgccgcca ccatggaatg gagttggata tttctctttc tcctgtcagg aactgcaggt 60
```

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gtccactctg aggtccagct gcagcagtct ggacctgagc tggtaaagcc tggggcttca 120
gtgaagatgt cctgcaaggc ttctggatac acattcacta gctatgttat gcactgggtg 180
aagcagaagc ctgggcaggg ccttgactgg attggatata ttgttcctta caatgatggc 240
actaagtaca atgagaagtt caaaggcaag gccacactga cttcagacaa atcctccagc 300
acagcctaca tggagctcag cagactgacc tctgaggact ctgcggtcta ttattgtgtc 360
tacggtagta ggtacgactg gtatttagat gtctggggcg cagggaccac ggtcaccgtc 420
tcctcagcta gcaccaaggg cccatcggtc ttccccctgg caccctcctc caagagcacc 480
tctgggggca cagcggccct gggctgcctg gtcaaggact acttccccga accggtgacg 540
gtgtcttgga actcaggcgc cctgaccagc ggcgtgcaca ccttcccggc tgtcctacag 600
tcctcaggac tctactccct cagcagcgtg gtgaccgtgc cctccagcag cttgggcacc 660
cagacctaca tctgcaacgt gaatcacaag cccagcaaca ccaaggtgga caagaaagtt 720
ggtgagaggc cagcacaggg agggagggtg tctgctggaa gcaggctcag cgctcctgcc 780
tggacgcatc ccggctatgc agccccagtc cagggcagca aggcaggccc cgtctgcctc 840
ttcacccgga gcctctgccc gccccactca tgctcaggga gagggtcttc tggctttttc 900
ccaggctctg ggcaggcaca ggctaggtgc ccctaaccca ggccctgcac acaaaggggc 960
aggtgctggg ctcagacctg ccaagagcca tatccgggag gaccctgccc ctgacctaag 1020
cccaccccaa aggccaaact ctccactccc tcagctcgga caccttctct cctcccagat 1080
tccagtaact cccaatcttc tctctgcaga gcccaaatct tgtgacaaaa ctcacacatg 1140
cccaccgtgc ccaggtaagc cagcccaggc ctcgccctcc agctcaaggc gggacaggtg 1200
ccctagagta gcctgcatcc agggacaggc cccagccggg tgctgacacg tccacctcca 1260
tctcttcctc agcacctgaa ctcctggggg gaccgtcagt cttcctcttc cccccaaaac 1320
ccaaggacac cctcatgatc tcccggaccc ctgaggtcac atgcgtggtg gtggacgtga 1380
gccacgaaga ccctgaggtc aagttcaact ggtacgtgga cggcgtggag gtgcataatg 1440
ccaagacaaa gccgcgggag gagcagtaca acagcacgta ccgggtggtc tgcgtcctca 1500
ccgtcctgca ccaggactgg ctgaatggca aggagtacaa gtgcaaggtc tccaacaaag 1560
ccctcccagc ccccatcgag aaaaccatct ccaaagccaa aggtgggacc cgtggggtgc 1620
gagggccaca tggacagagg ccggctcggc ccaccctctg ccctgagagt gaccgctgta 1680
ccaacctctg tcctacaggg cagccccgag aaccacaggt gtacaccctg cccccatccc 1740
gggatgagct gaccaagaac caggtcagcc tgacctgcct ggtcaaaggc ttctatccca 1800
gcgacatcgc cgtggagtgg gagagcaatg ggcagccgga gaacaactac aagaccacgc 1860
ctcccgtgct ggactccgac ggctccttct tcctctacag caagctcacc gtggacaaga 1920
gcaggtggca gcaggggaac gtcttctcat gctccgtgat gcatgaggct ctgcacaacc 1980
actacacgca gaagagcctc tccctgtctc ccggtaaatg a                     2021
```

```
<210> 12
<211> 468
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 12
Met Glu Trp Ser Trp Ile Phe Leu Phe Leu Leu Ser Gly Thr Ala Gly
 1               5                  10                   15
Val His Ser Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys
            20                  25                  30
Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe
        35                  40                  45
Thr Ser Tyr Val Met His Trp Val Lys Gln Lys Pro Gly Gln Gly Leu
    50                  55                  60
Asp Trp Ile Gly Tyr Ile Val Pro Tyr Asn Asp Gly Thr Lys Tyr Asn
65                  70                  75                  80
Glu Lys Phe Lys Gly Lys Ala Thr Leu Thr Ser Asp Lys Ser Ser Ser
                85                  90                  95
Thr Ala Tyr Met Glu Leu Ser Arg Leu Thr Ser Glu Asp Ser Ala Val
            100                 105                 110
```

```
Tyr Tyr Cys Val Tyr Gly Ser Arg Tyr Asp Trp Tyr Leu Asp Val Trp
        115                 120                 125
Gly Ala Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro
    130                 135                 140
Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr
145                 150                 155                 160
Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr
                165                 170                 175
Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro
            180                 185                 190
Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr
        195                 200                 205
Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn
    210                 215                 220
His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser
225                 230                 235                 240
Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
                245                 250                 255
Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
            260                 265                 270
Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
        275                 280                 285
His Glu Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Asp Gly Val Glu
    290                 295                 300
Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
305                 310                 315                 320
Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
                325                 330                 335
Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
            340                 345                 350
Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
        355                 360                 365
Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
    370                 375                 380
Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
385                 390                 395                 400
Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
                405                 410                 415
Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
            420                 425                 430
Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
        435                 440                 445
Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
    450                 455                 460
Ser Pro Gly Lys
465


<210> 13
<211> 786
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 13
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atcatcacca gaacagctta cgagcagacc gccagacagc tcacagggat caagcttgcc 60
gccaccatgg aatcacagac tcaggtcttc ctctccctgc tgctctgggt atctggtacc 120
tgtgggaaca ttatgatgac acagtcgcca tcatctctgg ctgtgtctgc aggagaaaag 180
gtcactatga gctgtaagtc cagtcaaagt gttttataca gttcaaatca gaagaactac 240
ttggcctggt accagcagaa accagggcag tctcctaaac tgctgatcta ctgggcatcc 300
actagggaat ctggtgtccc tgatcgcttc acaggcagtg gatctgggac agatttttact 360
cttaccatca gcagtgtaca agctgaagac ctggcagttt attactgtca tcaatatttc 420
tcctcataca cgttcggagg ggggaccaag ctggaaataa agcggactgt ggctgcacca 480
tctgtcttca tcttcccgcc atctgatgag cagttgaaat ctggaactgc ctctgttgtg 540
tgcctgctga ataacttcta tcccagagag gccaaagtac agtggaaggt ggataacgcc 600
ctccaatcgg gtaactccca ggagagtgtc acagagcagg acagcaagga cagcacctac 660
agcctcagca gcaccctgac gctgagcaaa gcagactacg agaaacacaa agtctacgcc 720
tgcgaagtca cccatcaggg cctgagctcg cccgtcacaa agagcttcaa caggggagag 780
tgttag                                                            786

<210> 14
<211> 239
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 14
Met Glu Ser Gln Thr Gln Val Phe Leu Ser Leu Leu Leu Trp Val Ser
 1               5                  10                  15
Gly Thr Cys Gly Asn Ile Met Met Thr Gln Ser Pro Ser Ser Leu Ala
            20                  25                      30
Val Ser Ala Gly Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser
        35                  40                      45
Val Leu Tyr Ser Ser Asn Gln Lys Asn Tyr Leu Ala Trp Tyr Gln Gln
    50                  55                      60
Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg
65                  70                      75              80
Glu Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp
                85                  90                  95
Phe Thr Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Val Tyr
            100                 105                 110
Tyr Cys His Gln Tyr Phe Ser Ser Tyr Thr Phe Gly Gly Gly Thr Lys
        115                 120                 125
Leu Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
    130                 135                 140
Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
145                 150                 155                 160
Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
                165                 170                 175
Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp
            180                 185                 190
Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
        195                 200                 205
Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln
    210                 215                 220
Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225                 230                 235


<210> 15
```

<211> 426
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 15
```
agagccgcca ccatggattg ggtgtggacc ttgctattcc tgttgtcagt aactgcaggt 60
gtccactccc aggtgcagct ggtgcagtct ggcggtggag tggtccagcc cggccgcagc 120
ctgaggctgt cctgcaaggc atctggctac accttcacca gctacgtgat gacatgggtg 180
cgccaagccc ccggaaaggg cctcgaatgg attggctaca ttgtgcctta taatgacggt 240
actaagtaca atgaaaagtt caagggcaga tttacaatat caagtgacaa gagcaagtca 300
accgcattcc tccaaatgga cagcttgcgt ccagaggaca ccgccgtata ctattgtgtg 360
cgcggcagcc gttacgactg gtacttggac tactggggcc aaggcactcc agtcaccgtc 420
tcctct                                                            426
```

<210> 16
<211> 138
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 16
```
Met Asp Trp Val Trp Thr Leu Leu Phe Leu Leu Ser Val Thr Ala Gly
1               5                   10                  15
Val His Ser Gln Val Gln Leu Val Gln Ser Gly Gly Gly Val Val Gln
            20                  25                  30
Pro Gly Arg Ser Leu Arg Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe
        35                  40                  45
Thr Ser Tyr Val Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
    50                  55                  60
Glu Trp Ile Gly Tyr Ile Val Pro Tyr Asn Asp Gly Thr Lys Tyr Asn
65                  70                  75                  80
Glu Lys Phe Lys Gly Arg Phe Thr Ile Ser Ser Asp Lys Ser Lys Ser
                85                  90                  95
Thr Ala Phe Leu Gln Met Asp Ser Leu Arg Pro Glu Asp Thr Ala Val
            100                 105                 110
Tyr Tyr Cys Ala Arg Gly Ser Arg Tyr Asp Trp Tyr Leu Asp Tyr Trp
        115                 120                 125
Gly Gln Gly Thr Pro Val Thr Val Ser Ser
    130                 135
```

<210> 17
<211> 465
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 17
```
gagcattacc ggccatactc atcaccatcc caggatatct ctagaaagct tgccgccacc 60
atggattttc aagtgcagat tttcagcttc ctgctaatca gtgcttcagt cataatgtcc 120
```

agaggaaaca tcatgatgac tcagagccca tccagcttga gcgcatcagt aggcgaccgc 180
gtaacgatca cttgcaaatc ctctcagtca gtattgtact ccagcaacca gaagaactac 240
ctggccggat atcagcagac tcccggcaaa gccccaaagt tgctgattta ttgggcctcc 300
acgcgcgagt ctggcgtgcc atcacgcttt agcggcagcg ggtccggtac agattacacg 360
tttaccatta gcagtctgca gcctgaggac atagccacct actactgtca ccagtacttt 420
agttcctaca cttttggcca gggaactaaa ctgcagatta ctcga 465

<210> 18
<211> 135
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 18
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
1 5 10 15
Val Ile Met Ser Arg Gly Asn Ile Met Met Thr Gln Ser Pro Ser Ser
20 25 30
Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ser Ser
35 40 45
Gln Ser Val Leu Tyr Ser Ser Asn Gln Lys Asn Tyr Leu Ala Trp Tyr
50 55 60
Gln Gln Thr Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Trp Ala Ser
65 70 75 80
Thr Arg Glu Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly
85 90 95
Thr Asp Tyr Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala
100 105 110
Thr Tyr Tyr Cys His Gln Tyr Phe Ser Ser Tyr Thr Phe Gly Gln Gly
115 120 125
Thr Lys Leu Gln Ile Thr Arg
130 135

<210> 19
<211> 2021
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 19
agagccgcca ccatggattg ggtgtggacc ttgctattcc tgttgtcagt aactgcaggt 60
gtccactccc aggtgcagct ggtgcagtct ggcggtggag tggtccagcc cggccgcagc 120
ctgaggctgt cctgcaaggc atctggctac accttcacca gctacgtgat gacatgggtg 180
cgccaagccc ccggaaaggg cctcgaatgg attggctaca ttgtgcctta taatgacggt 240
actaagtaca atgaaaagtt caagggcaga tttacaatat caagtgacaa gagcaagtca 300
accgcattcc tccaaatgga cagcttgcgt ccagaggaca ccgccgtata ctattgtgtg 360
cgcggcagcc gttacgactg gtacttggac tactggggcc aaggcactcc agtcaccgtc 420
tcctctgcta gcaccaaggg cccatcggtc ttccccctgg caccctcctc caagagcacc 480
tctgggggca cagcggccct gggctgcctg gtcaaggact acttccccga accggtgacg 540
gtgtcttgga actcaggcgc cctgaccagc ggcgtgcaca ccttcccggc tgtcctacag 600
tcctcaggac tctactccct cagcagcgtg gtgaccgtgc cctccagcag cttgggcacc 660
cagacctaca tctgcaacgt gaatcacaag cccagcaaca ccaaggtgga caagaaagtt 720

ggtgagaggc cagcacaggg agggagggtg tctgctggaa gcaggctcag cgctcctgcc 780
tggacgcatc ccggctatgc agccccagtc cagggcagca aggcaggccc cgtctgcctc 840
ttcacccgga gcctctgccc gccccactca tgctcaggga gagggtcttc tggctttttc 900
ccaggctctg ggcaggcaca ggctaggtgc ccctaaccca ggccctgcac acaaaggggc 960
aggtgctggg ctcagacctg ccaagagcca tatccgggag gaccctgccc ctgacctaag 1020
cccaccccaa aggccaaact ctccactccc tcagctcgga caccttctct cctcccagat 1080
tccagtaact cccaatcttc tctctgcaga gcccaaatct tgtgacaaaa ctcacacatg 1140
cccaccgtgc ccaggtaagc cagcccaggc ctcgccctcc agctcaaggc gggacaggtg 1200
ccctagagta gcctgcatcc agggacaggc cccagccggg tgctgacacg tccacctcca 1260
tctcttcctc agcacctgaa ctcctggggg gaccgtcagt cttcctcttc cccccaaaac 1320
ccaaggacac cctcatgatc tcccggaccc ctgaggtcac atgcgtggtg gtggacgtga 1380
gccacgaaga ccctgaggtc aagttcaact ggtacgtgga cggcgtggag gtgcataatg 1440
ccaagacaaa gccgcgggag gagcagtaca acagcacgta ccgggtggtc tgcgtcctca 1500
ccgtcctgca ccaggactgg ctgaatggca aggagtacaa gtgcaaggtc tccaacaaag 1560
ccctcccagc ccccatcgag aaaaccatct ccaaagccaa aggtgggacc cgtggggtgc 1620
gagggccaca tggacagagg ccggctcggc ccaccctctg ccctgagagt gaccgctgta 1680
ccaacctctg tcctacaggg cagccccgag aaccacaggt gtacaccctg cccccatccc 1740
gggatgagct gaccaagaac caggtcagcc tgacctgcct ggtcaaaggc ttctatccca 1800
gcgacatcgc cgtggagtgg gagagcaatg ggcagccgga gaacaactac aagaccacgc 1860
ctcccgtgct ggactccgac ggctccttct tcctctacag caagctcacc gtggacaaga 1920
gcaggtggca gcaggggaac gtcttctcat gctccgtgat gcatgaggct ctgcacaacc 1980
actacacgca gaagagcctc tccctgtctc ccggtaaatg a 2021

<210> 20
<211> 468
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 20
Met Asp Trp Val Trp Thr Leu Leu Phe Leu Leu Ser Val Thr Ala Gly
1 5 10 15
Val His Ser Gln Val Gln Leu Val Gln Ser Gly Gly Gly Val Val Gln
20 25 30
Pro Gly Arg Ser Leu Arg Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe
35 40 45
Thr Ser Tyr Val Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
50 55 60
Glu Trp Ile Gly Tyr Ile Val Pro Tyr Asn Asp Gly Thr Lys Tyr Asn
65 70 75 80
Glu Lys Phe Lys Gly Arg Phe Thr Ile Ser Ser Asp Lys Ser Lys Ser
85 90 95
Thr Ala Phe Leu Gln Met Asp Ser Leu Arg Pro Glu Asp Thr Ala Val
100 105 110
Tyr Tyr Cys Ala Arg Gly Ser Arg Tyr Asp Trp Tyr Leu Asp Tyr Trp
115 120 125
Gly Gln Gly Thr Pro Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro
130 135 140
Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr
145 150 155 160
Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr
165 170 175
Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro
180 185 190
Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr

```
        195                 200                 205
Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn
    210                 215                 220
His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser
225                 230                 235                 240
Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
                245                 250                 255
Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
            260                 265                 270
Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
        275                 280                 285
His Glu Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Asp Gly Val Glu
    290                 295                 300
Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
305                 310                 315                 320
Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
                325                 330                 335
Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
            340                 345                 350
Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
        355                 360                 365
Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
    370                 375                 380
Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
385                 390                 395                 400
Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
                405                 410                 415
Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
            420                 425                 430
Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
        435                 440                 445
Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
    450                 455                 460
Ser Pro Gly Lys
465


<210> 21
<211> 786
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 21
gagcattacc ggccatactc atcaccatcc caggatatct ctagaaagct tgccgccacc 60
atggattttc aagtgcagat tttcagcttc ctgctaatca gtgcttcagt cataatgtcc 120
agaggaaaca tcatgatgac tcagagccca tccagcttga gcgcatcagt aggcgaccgc 180
gtaacgatca cttgcaaatc ctctcagtca gtattgtact ccagcaacca gaagaactac 240
ctggccggat atcagcagac tcccggcaaa gccccaaagt tgctgattta ttgggcctcc 300
acgcgcgagt ctggcgtgcc atcacgcttt agcggcagcg ggtccggtac agattacacg 360
tttaccatta gcagtctgca gcctgaggac atagccacct actactgtca ccagtacttt 420
agttcctaca cttttggcca gggaactaaa ctgcagatta ctcgaactgt ggctgcacca 480
tctgtcttca tcttcccgcc atctgatgag cagttgaaat ctggaactgc ctctgttgtg 540
tgcctgctga ataacttcta tcccagagag gccaaagtac agtggaaggt ggataacgcc 600
ctccaatcgg gtaactccca ggagagtgtc acagagcagg acagcaagga cagcacctac 660
```

agcctcagca gcaccctgac gctgagcaaa gcagactacg agaaacacaa agtctacgcc 720
tgcgaagtca cccatcaggg cctgagctcg cccgtcacaa agagcttcaa caggggagag 780
tgttag 786

<210> 22
<211> 241
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 22

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Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1               5                  10                  15
Val Ile Met Ser Arg Gly Asn Ile Met Met Thr Gln Ser Pro Ser Ser
            20                  25                  30
Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ser Ser
        35                  40                  45
Gln Ser Val Leu Tyr Ser Ser Asn Gln Lys Asn Tyr Leu Ala Trp Tyr
    50                  55                  60
Gln Gln Thr Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Trp Ala Ser
65                  70                  75                  80
Thr Arg Glu Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly
                85                  90                  95
Thr Asp Tyr Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala
            100                 105                 110
Thr Tyr Tyr Cys His Gln Tyr Phe Ser Ser Tyr Thr Phe Gly Gln Gly
        115                 120                 125
Thr Lys Leu Gln Ile Thr Arg Thr Val Ala Ala Pro Ser Val Phe Ile
    130                 135                 140
Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val
145                 150                 155                 160
Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys
                165                 170                 175
Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu
            180                 185                 190
Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu
        195                 200                 205
Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr
    210                 215                 220
His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu
225                 230                 235                 240
Cys
```

<210> 23
<211> 2489
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 23
agagccgcca ccatggattg ggtgtggacc ttgctattcc tgttgtcagt aactgcaggt 60

```
gtccactccc aggtgcagct ggtgcagtct ggcggtggag tggtccagcc cggccgcagc 120
ctgaggctgt cctgcaaggc atctggctac accttcacca gctacgtgat gacatgggtg 180
cgccaagccc ccggaaaggg cctcgaatgg attggctaca ttgtgcctta taatgacggt 240
actaagtaca atgaaaagtt caagggcaga tttacaatat caagtgacaa gagcaagtca 300
accgcattcc tccaaatgga cagcttgcgt ccagaggaca ccgccgtata ctattgtgtg 360
cgcggcagcc gttacgactg gtacttggac tactggggcc aaggcactcc agtcaccgtc 420
tcctctgcta gcaccaaggg cccatcggtc ttccccctgg caccctcctc caagagcacc 480
tctgggggca cagcggccct gggctgcctg gtcaaggact acttccccga accggtgacg 540
gtgtcttgga actcaggcgc cctgaccagc ggcgtgcaca ccttcccggc tgtcctacag 600
tcctcaggac tctactccct cagcagcgtg gtgaccgtgc cctccagcag cttgggcacc 660
cagacctaca tctgcaacgt gaatcacaag cccagcaaca ccaaggtgga caagaaagtt 720
ggtgagaggc cagcacaggg agggagggtg tctgctggaa gcaggctcag cgctcctgcc 780
tggacgcatc ccggctatgc agccccagtc cagggcagca aggcaggccc cgtctgcctc 840
ttcacccgga gcctctgccc gccccactca tgctcaggga gagggtcttc tggctttttc 900
ccaggctctg ggcaggcaca ggctaggtgc ccctaaccca ggccctgcac acaaaggggc 960
aggtgctggg ctcagacctg ccaagagcca tatccgggag gaccctgccc ctgacctaag 1020
cccaccccaa aggccaaact ctccactccc tcagctcgga caccttctct cctcccagat 1080
tccagtaact cccaatcttc tctctgcaga gcccaaatct tgtgacaaaa ctcacacatg 1140
cccaccgtgc ccaggtaagc cagcccaggc ctcgccctcc agctcaaggc gggacaggtg 1200
ccctagagta gcctgcatcc agggacaggc cccagccggg tgctgacacg tccacctcca 1260
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ccaaggacac cctcatgatc tcccggaccc ctgaggtcac atgcgtggtg gtggacgtga 1380
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ccaagacaaa gccgcgggag gagcagtaca acagcacgta ccgggtggtc tgcgtcctca 1500
ccgtcctgca ccaggactgg ctgaatggca aggagtacaa gtgcaaggtc tccaacaaag 1560
ccctcccagc ccccatcgag aaaaccatct ccaaagccaa aggtgggacc cgtggggtgc 1620
gagggccaca tggacagagg ccggctcggc ccaccctctg ccctgagagt gaccgctgta 1680
ccaacctctg tcctacaggg cagccccgag aaccacaggt gtacaccctg cccccatccc 1740
gggatgagct gaccaagaac caggtcagcc tgacctgcct ggtcaaaggc ttctatccca 1800
gcgacatcgc cgtggagtgg gagagcaatg ggcagccgga gaacaactac aagaccacgc 1860
ctcccgtgct ggactccgac ggctccttct tcctctacag caagctcacc gtggacaaga 1920
gcaggtggca gcaggggaac gtcttctcat gctccgtgat gcatgaggct ctgcacaacc 1980
actacacgca gaagagcctc tccctgtctc ccggtaaaac ccaggactgc tccttccaac 2040
acagccccat ctcctccgac ttcgctgtca aaatccgtga gctgtctgac tacctgcttc 2100
aagattaccc agtcaccgtg gcctccaacc tgcaggacga ggagctctgc gggggcctct 2160
ggcggctggt cctggcacag cgctggatgg agcggctcaa gactgtcgct gggtccaaga 2220
tgcaaggctt gctggagcgc gtgaacacgg agatacactt tgtcaccaaa tgtgcctttc 2280
agcccccccc cagctgtctt cgcttcgtcc agaccaacat ctcccgcctc ctgcaggaga 2340
cctccgagca gctggtggcg ctgaagccct ggatcactcg ccagaacttc tcccggtgcc 2400
tggagctgca gtgtcagccc gactcctcaa ccctgccacc cccatggagt ccccggcccc 2460
tggaggccac agccccgaca gccccgtga                                   2489
```

<210> 24
<211> 624
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 24

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Met Asp Trp Val Trp Thr Leu Leu Phe Leu Leu Ser Val Thr Ala Gly
 1               5                   10                  15
Val His Ser Gln Val Gln Leu Val Gln Ser Gly Gly Gly Val Val Gln
            20                  25                  30
Pro Gly Arg Ser Leu Arg Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe
        35                  40                  45
```

```
Thr Ser Tyr Val Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
    50                  55                  60
Glu Trp Ile Gly Tyr Ile Val Pro Tyr Asn Asp Gly Thr Lys Tyr Asn
65                  70                  75                  80
Glu Lys Phe Lys Gly Arg Phe Thr Ile Ser Ser Asp Lys Ser Lys Ser
                85                  90                  95
Thr Ala Phe Leu Gln Met Asp Ser Leu Arg Pro Glu Asp Thr Ala Val
            100                 105                 110
Tyr Tyr Cys Ala Arg Gly Ser Arg Tyr Asp Trp Tyr Leu Asp Tyr Trp
        115                 120                 125
Gly Gln Gly Thr Pro Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro
    130                 135                 140
Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr
145                 150                 155                 160
Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr
                165                 170                 175
Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro
            180                 185                 190
Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr
        195                 200                 205
Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn
    210                 215                 220
His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser
225                 230                 235                 240
Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
                245                 250                 255
Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
            260                 265                 270
Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
        275                 280                 285
His Glu Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Asp Gly Val Glu
    290                 295                 300
Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
305                 310                 315                 320
Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
                325                 330                 335
Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
            340                 345                 350
Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
        355                 360                 365
Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
    370                 375                 380
Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
385                 390                 395                 400
Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
                405                 410                 415
Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
            420                 425                 430
Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
        435                 440                 445
Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
    450                 455                 460
Ser Pro Gly Lys Thr Gln Asp Cys Ser Phe Gln His Ser Pro Ile Ser
465                 470                 475                 480
Ser Asp Phe Ala Val Lys Ile Arg Glu Leu Ser Asp Tyr Leu Leu Gln
                485                 490                 495
Asp Tyr Pro Val Thr Val Ala Ser Asn Leu Gln Asp Glu Glu Leu Cys
```

```
            500                 505                 510
Gly Gly Leu Trp Arg Leu Val Leu Ala Gln Arg Trp Met Glu Arg Leu
        515                 520                 525
Lys Thr Val Ala Gly Ser Lys Met Gln Gly Leu Leu Glu Arg Val Asn
    530                 535                 540
Thr Glu Ile His Phe Val Thr Lys Cys Ala Phe Gln Pro Pro Pro Ser
545                 550                 555                 560
Cys Leu Arg Phe Val Gln Thr Asn Ile Ser Arg Leu Leu Gln Glu Thr
                565                 570                 575
Ser Glu Gln Leu Val Ala Leu Lys Pro Trp Ile Thr Arg Gln Asn Phe
            580                 585                 590
Ser Arg Cys Leu Glu Leu Gln Cys Gln Pro Asp Ser Ser Thr Leu Pro
        595                 600                 605
Pro Pro Trp Ser Pro Arg Pro Leu Glu Ala Thr Ala Pro Thr Ala Pro
    610                 615                 620
```

<210> 25
<211> 2534
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 25

```
agagccgcca ccatggattg ggtgtggacc ttgctattcc tgttgtcagt aactgcaggt 60
gtccactccc aggtgcagct ggtgcagtct ggcggtggag tggtccagcc cggccgcagc 120
ctgaggctgt cctgcaaggc atctggctac accttcacca gctacgtgat gacatgggtg 180
cgccaagccc ccggaaaggg cctcgaatgg attggctaca ttgtgcctta taatgacggt 240
actaagtaca atgaaaagtt caagggcaga tttacaatat caagtgacaa gagcaagtca 300
accgcattcc tccaaatgga cagcttgcgt ccagaggaca ccgccgtata ctattgtgtg 360
cgcggcagcc gttacgactg gtacttggac tactggggcc aaggcactcc agtcaccgtc 420
tcctctgcta gcaccaaggg cccatcggtc ttccccctgg caccctcctc caagagcacc 480
tctgggggca cagcggccct gggctgcctg gtcaaggact acttccccga accggtgacg 540
gtgtcttgga actcaggcgc cctgaccagc ggcgtgcaca ccttcccggc tgtcctacag 600
tcctcaggac tctactccct cagcagcgtg gtgaccgtgc cctccagcag cttgggcacc 660
cagacctaca tctgcaacgt gaatcacaag cccagcaaca ccaaggtgga caagaaagtt 720
ggtgagaggc cagcacaggg agggagggtg tctgctggaa gcaggctcag cgctcctgcc 780
tggacgcatc ccggctatgc agccccagtc cagggcagca aggcaggccc cgtctgcctc 840
ttcacccgga gcctctgccc gccccactca tgctcaggga gagggtcttc tggctttttc 900
ccaggctctg ggcaggcaca ggctaggtgc ccctaaccca ggccctgcac acaaaggggc 960
aggtgctggg ctcagacctg ccaagagcca tatccgggag gaccctgccc ctgacctaag 1020
cccaccccaa aggccaaact ctccactccc tcagctcgga caccttctct cctcccagat 1080
tccagtaact cccaatcttc tctctgcaga gcccaaatct tgtgacaaaa ctcacacatg 1140
cccaccgtgc ccaggtaagc cagcccaggc ctcgccctcc agctcaaggc gggacaggtg 1200
ccctagagta gcctgcatcc agggacaggc cccagccggg tgctgacacg tccacctcca 1260
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ccaaggacac cctcatgatc tcccggaccc ctgaggtcac atgcgtggtg gtggacgtga 1380
gccacgaaga ccctgaggtc aagttcaact ggtacgtgga cggcgtggag gtgcataatg 1440
ccaagacaaa gccgcgggag gagcagtaca acagcacgta ccgggtggtc tgcgtcctca 1500
ccgtcctgca ccaggactgg ctgaatggca aggagtacaa gtgcaaggtc tccaacaaag 1560
ccctcccagc ccccatcgag aaaaccatct ccaaagccaa aggtgggacc cgtggggtgc 1620
gagggccaca tggacagagg ccggctcggc ccaccctctg ccctgagagt gaccgctgta 1680
ccaacctctg tcctacaggg cagccccgag aaccacaggt gtacaccctg cccccatccc 1740
gggatgagct gaccaagaac caggtcagcc tgacctgcct ggtcaaaggc ttctatccca 1800
gcgacatcgc cgtggagtgg gagagcaatg ggcagccgga gaacaactac aagaccacgc 1860
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ctcccgtgct ggactccgac ggctccttct tcctctacag caagctcacc gtggacaaga 1920
gcaggtggca gcaggggaac gtcttctcat gctccgtgat gcatgaggct ctgcacaacc 1980
actacacgca gaagagcctc tccctgtctc ccggtaaagg cggtggaggc tctggtggag 2040
gcggttcagg aggcggtgga tctacccagg actgctcctt ccaacacagc cccatctcct 2100
ccgacttcgc tgtcaaaatc cgtgagctgt ctgactacct gcttcaagat tacccagtca 2160
ccgtggcctc caacctgcag gacgaggagc tctgcggggg cctctggcgg ctggtcctgg 2220
cacagcgctg gatggagcgg ctcaagactg tcgctgggtc caagatgcaa ggcttgctgg 2280
agcgcgtgaa cacggagata cactttgtca ccaaatgtgc ctttcagccc ccccccagct 2340
gtcttcgctt cgtccagacc aacatctccc gcctcctgca ggagacctcc gagcagctgg 2400
tggcgctgaa gccctggatc actcgccaga acttctcccg gtgcctggag ctgcagtgtc 2460
agcccgactc ctcaaccctg ccacccccat ggagtccccg gcccctggag gccacagccc 2520
cgacagcccc gtga                                                   2534

<210> 26
<211> 639
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 26
Met Asp Trp Val Trp Thr Leu Leu Phe Leu Leu Ser Val Thr Ala Gly
 1               5                  10                  15
Val His Ser Gln Val Gln Leu Val Gln Ser Gly Gly Gly Val Val Gln
            20                  25                  30
Pro Gly Arg Ser Leu Arg Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe

        35                  40                  45
Thr Ser Tyr Val Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
    50                  55                  60
Glu Trp Ile Gly Tyr Ile Val Pro Tyr Asn Asp Gly Thr Lys Tyr Asn
65                  70                  75                  80
Glu Lys Phe Lys Gly Arg Phe Thr Ile Ser Ser Asp Lys Ser Lys Ser
                85                  90                  95
Thr Ala Phe Leu Gln Met Asp Ser Leu Arg Pro Glu Asp Thr Ala Val
            100                 105                 110
Tyr Tyr Cys Ala Arg Gly Ser Arg Tyr Asp Trp Tyr Leu Asp Tyr Trp
        115                 120                 125
Gly Gln Gly Thr Pro Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro
    130                 135                 140
Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr
145                 150                 155                 160
Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr
                165                 170                 175
Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro
            180                 185                 190
Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr
        195                 200                 205
Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn
    210                 215                 220
His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser
225                 230                 235                 240
Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
                245                 250                 255
Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
            260                 265                 270
```

```
Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
        275                 280                 285
His Glu Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Asp Gly Val Glu
    290                 295                 300
Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
305                 310                 315                 320
Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
                325                 330                 335
Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
            340                 345                 350
Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
        355                 360                 365
Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
    370                 375                 380
Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
385                 390                 395                 400
Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
                405                 410                 415
Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
            420                 425                 430
Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
        435                 440                 445
Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
    450                 455                 460
Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
465                 470                 475                 480
Gly Gly Ser Thr Gln Asp Cys Ser Phe Gln His Ser Pro Ile Ser Ser
                485                 490                 495
Asp Phe Ala Val Lys Ile Arg Glu Leu Ser Asp Tyr Leu Leu Gln Asp
            500                 505                 510
Tyr Pro Val Thr Val Ala Ser Asn Leu Gln Asp Glu Glu Leu Cys Gly
        515                 520                 525
Gly Leu Trp Arg Leu Val Leu Ala Gln Arg Trp Met Glu Arg Leu Lys
    530                 535                 540
Thr Val Ala Gly Ser Lys Met Gln Gly Leu Leu Glu Arg Val Asn Thr
545                 550                 555                 560
Glu Ile His Phe Val Thr Lys Cys Ala Phe Gln Pro Pro Pro Ser Cys
                565                 570                 575
Leu Arg Phe Val Gln Thr Asn Ile Ser Arg Leu Leu Gln Glu Thr Ser
            580                 585                 590
Glu Gln Leu Val Ala Leu Lys Pro Trp Ile Thr Arg Gln Asn Phe Ser
        595                 600                 605
Arg Cys Leu Glu Leu Gln Cys Gln Pro Asp Ser Ser Thr Leu Pro Pro
    610                 615                 620
Pro Trp Ser Pro Arg Pro Leu Glu Ala Thr Ala Pro Thr Ala Pro
625                 630                 635
```

<210> 27
<211> 1986
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 27

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agctcgggac tcagtgggac ccaggactgc tccttccaac acagccccat ctcctccgac 120
ttcgctgtca aaatccgtga gctgtctgac tacctgcttc aagattaccc agtcaccgtg 180
gcctccaacc tgcaggacga ggagctctgc gggggcctct ggcggctggt cctggcacag 240
cgctggatgg agcggctcaa gactgtcgct gggtccaaga tgcaaggctt gctggagcgc 300
gtgaacacgg agatacactt tgtcaccaaa tgtgcctttc agcccccccc cagctgtctt 360
cgcttcgtcc agaccaacat ctcccgcctc ctgcaggaga cctccgagca gctggtggcg 420
ctgaagccct ggatcactcg ccagaacttc tcccggtgcc tggagctgca gtgtcagccc 480
gactcctcaa ccctgccacc cccatggagt ccccggcccc tggaggccac agccccgaca 540
gccccggagc ccaaatcttg tgacaaaact cacacatgcc caccgtgccc agcacctgaa 600
ctcctggggg gaccgtcagt cttcctcttc cccccaaaac ccaaggacac cctcatgatc 660
tcccggaccc ctgaggtcac atgcgtggtg gtggacgtga gccacgaaga ccctgaggtc 720
aagttcaact ggtacgtgga cggcgtggag gtgcataatg ccaagacaaa gccgcgggag 780
gagcagtaca acagcacgta ccgggtggtc tgcgtcctca ccgtcctgca ccaggactgg 840
ctgaatggca aggagtacaa gtgcaaggtc tccaacaaag ccctcccagc ccccatcgag 900
aaaaccatct ccaaagccaa agggcagccc cgagaaccac aggtgtacac cctgccccca 960
tcccgggatg agctgaccaa gaaccaggtc agcctgacct gcctggtcaa aggcttctat 1020
cccagcgaca tcgccgtgga gtgggagagc aatgggcagc cggagaacaa ctacaagacc 1080
acgcctcccg tgctggactc cgacggctcc ttcttcctct acagcaagct caccgtggac 1140
aagagcaggt ggcagcaggg gaacgtcttc tcatgctccg tgatgcatga ggctctgcac 1200
aaccactaca cgcagaagag cctctccctg tctccgggta aacaggtgca gctggtgcag 1260
tctggcggtg gagtggtcca gcccggccgc agcctgaggc tgtcctgcaa ggcatctggc 1320
tacaccttca ccagctacgt gatgacatgg gtgcgccaag cccccggaaa gggcctcgaa 1380
tggattggct acattgtgcc ttataatgac ggtactaagt acaatgaaaa gttcaagggc 1440
agatttacaa tatcaagtga caagagcaag tcaaccgcat tcctccaaat ggacagcttg 1500
cgtccagagg acaccgccgt atactattgt gtgcgcggca gccgttacga ctggtacttg 1560
gactactggg gccaaggcac tccagtcacc gtctcctctg gcggtggagg ctctggtgga 1620
ggcggttcag gaggcggtgg atctaacatc atgatgactc agagcccatc cagcttgagc 1680
gcatcagtag gcgaccgcgt aacgatcact tgcaaatcct ctcagtcagt attgtactcc 1740
agcaaccaga agaactacct ggccggatat cagcagactc ccggcaaagc cccaaagttg 1800
ctgatttatt gggcctccac gcgcgagtct ggcgtgccat cacgctttag cggcagcggg 1860
tccggtacag attacacgtt taccattagc agtctgcagc ctgaggacat agccacctac 1920
tactgtcacc agtactttag ttcctacact tttggccagg gaactaaact gcagattact 1980
cgatga                                                            1986

<210> 28
<211> 661
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 28
Met Thr Val Leu Ala Pro Ala Trp Ser Pro Thr Thr Tyr Leu Leu Leu
 1               5                  10                  15
Leu Leu Leu Leu Ser Ser Gly Leu Ser Gly Thr Gln Asp Cys Ser Phe
            20                  25                  30
Gln His Ser Pro Ile Ser Ser Asp Phe Ala Val Lys Ile Arg Glu Leu
        35                  40                  45
Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val Thr Val Ala Ser Asn Leu
    50                  55                  60
Gln Asp Glu Glu Leu Cys Gly Gly Leu Trp Arg Leu Val Leu Ala Gln
65                  70                  75                  80
Arg Trp Met Glu Arg Leu Lys Thr Val Ala Gly Ser Lys Met Gln Gly
                85                  90                  95
Leu Leu Glu Arg Val Asn Thr Glu Ile His Phe Val Thr Lys Cys Ala
```

```
            100                 105                 110
Phe Gln Pro Pro Pro Ser Cys Leu Arg Phe Val Gln Thr Asn Ile Ser
        115                 120                 125
Arg Leu Leu Gln Glu Thr Ser Glu Gln Leu Val Ala Leu Lys Pro Trp
    130                 135                 140
Ile Thr Arg Gln Asn Phe Ser Arg Cys Leu Glu Leu Gln Cys Gln Pro
145                 150                 155                 160
Asp Ser Ser Thr Leu Pro Pro Pro Trp Ser Pro Arg Pro Leu Glu Ala
                165                 170                 175
Thr Ala Pro Thr Ala Pro Glu Pro Lys Ser Cys Asp Lys Thr His Thr
            180                 185                 190
Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe
        195                 200                 205
Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
    210                 215                 220
Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
225                 230                 235                 240
Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
                245                 250                 255
Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
            260                 265                 270
Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
        275                 280                 285
Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
    290                 295                 300
Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
305                 310                 315                 320
Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
                325                 330                 335
Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
            340                 345                 350
Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
        355                 360                 365
Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
    370                 375                 380
Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
385                 390                 395                 400
Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Gln Val
                405                 410                 415
Gln Leu Val Gln Ser Gly Gly Gly Val Val Gln Pro Gly Arg Ser Leu
            420                 425                 430
Arg Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr Val Met
        435                 440                 445
His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Ile Gly Tyr
    450                 455                 460
Ile Val Pro Tyr Asn Asp Gly Thr Lys Tyr Asn Glu Lys Phe Lys Gly
465                 470                 475                 480
Arg Phe Thr Ile Ser Ser Asp Lys Ser Lys Ser Thr Ala Phe Leu Gln
                485                 490                 495
Met Asp Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg
            500                 505                 510
Gly Ser Arg Tyr Asp Trp Tyr Leu Asp Tyr Trp Gly Gln Gly Thr Pro
        515                 520                 525
Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
    530                 535                 540
Gly Gly Gly Ser Asn Ile Met Met Thr Gln Ser Pro Ser Ser Leu Ser
545                 550                 555                 560
```

```
Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ser Ser Gln Ser
                565                 570                 575
Val Leu Tyr Ser Ser Asn Gln Lys Asn Tyr Leu Ala Trp Tyr Gln Gln
            580                 585                 590
Thr Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg
    595                 600                 605
Glu Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
    610                 615                 620
Tyr Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr
625                 630                 635                 640
Tyr Cys His Gln Tyr Phe Ser Ser Tyr Thr Phe Gly Gln Gly Thr Lys
                645                 650                 655
Leu Gln Ile Thr Arg
            660
```

<210> 29
<211> 2489
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 29

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cttgccgcca ccatggaatg gagttggata tttctctttc tcctgtcagg aactgcaggt 60
gtccactctg aggtccagct gcagcagtct ggacctgagc tggtaaagcc tggggcttca 120
gtgaagatgt cctgcaaggc ttctggatac acattcacta gctatgttat gcactgggtg 180
aagcagaagc ctgggcaggg ccttgactgg attggatata ttgttcctta caatgatggc 240
actaagtaca atgagaagtt caaaggcaag gccacactga cttcagacaa atcctccagc 300
acagcctaca tggagctcag cagactgacc tctgaggact ctgcggtcta ttattgtgtc 360
tacggtagta ggtacgactg gtatttagat gtctggggcg cagggaccac ggtcaccgtc 420
tcctcagcta gcaccaaggg cccatcggtc ttccccctgg caccctcctc caagagcacc 480
tctgggggca cagcggccct gggctgcctg gtcaaggact acttccccga accggtgacg 540
gtgtcttgga actcaggcgc cctgaccagc ggcgtgcaca ccttcccggc tgtcctacag 600
tcctcaggac tctactccct cagcagcgtg gtgaccgtgc cctccagcag cttgggcacc 660
cagacctaca tctgcaacgt gaatcacaag cccagcaaca ccaaggtgga caagaaagtt 720
ggtgagaggc cagcacaggg agggagggtg tctgctggaa gcaggctcag cgctcctgcc 780
tggacgcatc ccggctatgc agccccagtc cagggcagca aggcaggccc cgtctgcctc 840
ttcacccgga gcctctgccc gccccactca tgctcaggga gagggtcttc tggctttttc 900
ccaggctctg ggcaggcaca ggctaggtgc ccctaaccca ggccctgcac acaaaggggc 960
aggtgctggg ctcagacctg ccaagagcca tatccgggag gaccctgccc ctgacctaag 1020
cccaccccaa aggccaaact ctccactccc tcagctcgga caccttctct cctcccagat 1080
tccagtaact cccaatcttc tctctgcaga gcccaaatct tgtgacaaaa ctcacacatg 1140
cccaccgtgc ccaggtaagc cagcccaggc ctcgccctcc agctcaaggc gggacaggtg 1200
ccctagagta gcctgcatcc agggacaggc cccagccggg tgctgacacg tccacctcca 1260
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ccaaggacac cctcatgatc tcccggaccc ctgaggtcac atgcgtggtg gtggacgtga 1380
gccacgaaga ccctgaggtc aagttcaact ggtacgtgga cggcgtggag gtgcataatg 1440
ccaagacaaa gccgcgggag gagcagtaca acagcacgta ccgggtggtc tgcgtcctca 1500
ccgtcctgca ccaggactgg ctgaatggca aggagtacaa gtgcaaggtc tccaacaaag 1560
ccctcccagc ccccatcgag aaaaccatct ccaaagccaa aggtgggacc cgtggggtgc 1620
gagggccaca tggacagagg ccggctcggc ccaccctctg ccctgagagt gaccgctgta 1680
ccaacctctg tcctacaggg cagccccgag aaccacaggt gtacaccctg cccccatccc 1740
gggatgagct gaccaagaac caggtcagcc tgacctgcct ggtcaaaggc ttctatccca 1800
gcgacatcgc cgtggagtgg gagagcaatg ggcagccgga gaacaactac aagaccacgc 1860
ctcccgtgct ggactccgac ggctccttct tcctctacag caagctcacc gtggacaaga 1920
```

gcaggtggca gcaggggaac gtcttctcat gctccgtgat gcatgaggct ctgcacaacc 1980
actacacgca gaagagcctc tccctgtctc ccggtaaaac ccaggactgc tccttccaac 2040
acagccccat ctcctccgac ttcgctgtca aaatccgtga gctgtctgac tacctgcttc 2100
aagattaccc agtcaccgtg gcctccaacc tgcaggacga ggagctctgc gggggcctct 2160
ggcggctggt cctggcacag cgctggatgg agcggctcaa gactgtcgct gggtccaaga 2220
tgcaaggctt gctggagcgc gtgaacacgg agatacactt tgtcaccaaa tgtgcctttc 2280
agcccccccc cagctgtctt cgcttcgtcc agaccaacat ctcccgcctc ctgcaggaga 2340
cctccgagca gctggtggcg ctgaagccct ggatcactcg ccagaacttc tcccggtgcc 2400
tggagctgca gtgtcagccc gactcctcaa ccctgccacc cccatggagt ccccggcccc 2460
tggaggccac agccccgaca gccccgtga 2489

<210> 30
<211> 624
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 30
Met Glu Trp Ser Trp Ile Phe Leu Phe Leu Leu Ser Gly Thr Ala Gly
 1   5   10   15
Val His Ser Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys
             20   25   30
Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe
         35   40   45
Thr Ser Tyr Val Met His Trp Val Lys Gln Lys Pro Gly Gln Gly Leu
     50   55   60
Asp Trp Ile Gly Tyr Ile Val Pro Tyr Asn Asp Gly Thr Lys Tyr Asn
65   70   75   80
Glu Lys Phe Lys Gly Lys Ala Thr Leu Thr Ser Asp Lys Ser Ser Ser
                 85   90   95
Thr Ala Tyr Met Glu Leu Ser Arg Leu Thr Ser Glu Asp Ser Ala Val
            100   105   110
Tyr Tyr Cys Val Tyr Gly Ser Arg Tyr Asp Trp Tyr Leu Asp Val Trp
        115   120   125
Gly Ala Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro
    130   135   140
Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr
145   150   155   160
Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr
                165   170   175
Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro
            180   185   190
Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr
        195   200   205
Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn
    210   215   220
His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser
225   230   235   240
Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
                245   250   255
Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
            260   265   270
Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
        275   280   285
His Glu Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Asp Gly Val Glu

```
    290                 295                 300
Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
305                 310                 315                 320
Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
                325                 330                 335
Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
            340                 345                 350
Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
        355                 360                 365
Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
    370                 375                 380
Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
385                 390                 395                 400
Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
                405                 410                 415
Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
            420                 425                 430
Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
        435                 440                 445
Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
    450                 455                 460
Ser Pro Gly Lys Thr Gln Asp Cys Ser Phe Gln His Ser Pro Ile Ser
465                 470                 475                 480
Ser Asp Phe Ala Val Lys Ile Arg Glu Leu Ser Asp Tyr Leu Leu Gln
                485                 490                 495
Asp Tyr Pro Val Thr Val Ala Ser Asn Leu Gln Asp Glu Glu Leu Cys
            500                 505                 510
Gly Gly Leu Trp Arg Leu Val Leu Ala Gln Arg Trp Met Glu Arg Leu
        515                 520                 525
Lys Thr Val Ala Gly Ser Lys Met Gln Gly Leu Leu Glu Arg Val Asn
    530                 535                 540
Thr Glu Ile His Phe Val Thr Lys Cys Ala Phe Gln Pro Pro Pro Ser
545                 550                 555                 560
Cys Leu Arg Phe Val Gln Thr Asn Ile Ser Arg Leu Leu Gln Glu Thr
                565                 570                 575
Ser Glu Gln Leu Val Ala Leu Lys Pro Trp Ile Thr Arg Gln Asn Phe
            580                 585                 590
Ser Arg Cys Leu Glu Leu Gln Cys Gln Pro Asp Ser Ser Thr Leu Pro
        595                 600                 605
Pro Pro Trp Ser Pro Arg Pro Leu Glu Ala Thr Ala Pro Thr Ala Pro
    610                 615                 620


<210> 31
<211> 2534
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 31
cttgccgcca ccatggaatg gagttggata tttctctttc tcctgtcagg aactgcaggt 60
gtccactctg aggtccagct gcagcagtct ggacctgagc tggtaaagcc tggggcttca 120
gtgaagatgt cctgcaaggc ttctggatac acattcacta gctatgttat gcactgggtg 180
aagcagaagc ctgggcaggg ccttgactgg attggatata ttgttcctta caatgatggc 240
actaagtaca atgagaagtt caaaggcaag gccacactga cttcagacaa atcctccagc 300
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acagcctaca tggagctcag cagactgacc tctgaggact ctgcggtcta ttattgtgtc 360
tacggtagta ggtacgactg gtatttagat gtctggggcg cagggaccac ggtcaccgtc 420
tcctcagcta gcaccaaggg cccatcggtc ttccccctgg caccctcctc caagagcacc 480
tctgggggca cagcggccct gggctgcctg gtcaaggact acttccccga accggtgacg 540
gtgtcttgga actcaggcgc cctgaccagc ggcgtgcaca ccttcccggc tgtcctacag 600
tcctcaggac tctactccct cagcagcgtg gtgaccgtgc cctccagcag cttgggcacc 660
cagacctaca tctgcaacgt gaatcacaag cccagcaaca ccaaggtgga caagaaagtt 720
ggtgagaggc cagcacaggg agggagggtg tctgctggaa gcaggctcag cgctcctgcc 780
tggacgcatc ccggctatgc agccccagtc cagggcagca aggcaggccc cgtctgcctc 840
ttcacccgga gcctctgccc gccccactca tgctcaggga gagggtcttc tggctttttc 900
ccaggctctg ggcaggcaca ggctaggtgc ccctaaccca ggccctgcac acaaaggggc 960
aggtgctggg ctcagacctg ccaagagcca tatccgggag gaccctgccc ctgacctaag 1020
cccaccccaa aggccaaact ctccactccc tcagctcgga caccttctct cctcccagat 1080
tccagtaact cccaatcttc tctctgcaga gcccaaatct tgtgacaaaa ctcacacatg 1140
cccaccgtgc ccaggtaagc cagcccaggc ctcgccctcc agctcaaggc gggacaggtg 1200
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ccaaggacac cctcatgatc tcccggaccc ctgaggtcac atgcgtggtg gtggacgtga 1380
gccacgaaga ccctgaggtc aagttcaact ggtacgtgga cggcgtggag gtgcataatg 1440
ccaagacaaa gccgcgggag gagcagtaca acagcacgta ccgggtggtc tgcgtcctca 1500
ccgtcctgca ccaggactgg ctgaatggca aggagtacaa gtgcaaggtc tccaacaaag 1560
ccctcccagc ccccatcgag aaaaccatct ccaaagccaa aggtgggacc cgtggggtgc 1620
gagggccaca tggacagagg ccggctcggc ccaccctctg ccctgagagt gaccgctgta 1680
ccaacctctg tcctacaggg cagccccgag aaccacaggt gtacaccctg cccccatccc 1740
gggatgagct gaccaagaac caggtcagcc tgacctgcct ggtcaaaggc ttctatccca 1800
gcgacatcgc cgtggagtgg gagagcaatg ggcagccgga gaacaactac aagaccacgc 1860
ctcccgtgct ggactccgac ggctccttct tcctctacag caagctcacc gtggacaaga 1920
gcaggtggca gcaggggaac gtcttctcat gctccgtgat gcatgaggct ctgcacaacc 1980
actacacgca gaagagcctc tccctgtctc ccggtaaagg cggtggaggc tctggtggag 2040
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ccgacttcgc tgtcaaaatc cgtgagctgt ctgactacct gcttcaagat tacccagtca 2160
ccgtggcctc caacctgcag gacgaggagc tctgcggggg cctctggcgg ctggtcctgg 2220
cacagcgctg gatggagcgg ctcaagactg tcgctgggtc caagatgcaa ggcttgctgg 2280
agcgcgtgaa cacggagata cactttgtca ccaaatgtgc ctttcagccc ccccccagct 2340
gtcttcgctt cgtccagacc aacatctccc gcctcctgca ggagacctcc gagcagctgg 2400
tggcgctgaa gccctggatc actcgccaga acttctcccg gtgcctggag ctgcagtgtc 2460
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cgacagcccc gtga                                                   2534

<210> 32
<211> 639
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 32
Met Glu Trp Ser Trp Ile Phe Leu Phe Leu Leu Ser Gly Thr Ala Gly
 1               5                  10                  15
Val His Ser Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys
            20                  25                  30
Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe
        35                  40                  45
Thr Ser Tyr Val Met His Trp Val Lys Gln Lys Pro Gly Gln Gly Leu
    50                  55                  60
Asp Trp Ile Gly Tyr Ile Val Pro Tyr Asn Asp Gly Thr Lys Tyr Asn
```

```
65                  70                  75                  80
Glu Lys Phe Lys Gly Lys Ala Thr Leu Thr Ser Asp Lys Ser Ser Ser
                85                  90                  95
Thr Ala Tyr Met Glu Leu Ser Arg Leu Thr Ser Glu Asp Ser Ala Val
            100                 105                 110
Tyr Tyr Cys Val Tyr Gly Ser Arg Tyr Asp Trp Tyr Leu Asp Val Trp
        115                 120                 125
Gly Ala Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro
    130                 135                 140
Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr
145                 150                 155                 160
Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr
                165                 170                 175
Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro
            180                 185                 190
Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr
        195                 200                 205
Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn
    210                 215                 220
His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser
225                 230                 235                 240
Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
                245                 250                 255
Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
            260                 265                 270
Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
        275                 280                 285
His Glu Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Asp Gly Val Glu
    290                 295                 300
Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
305                 310                 315                 320
Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
                325                 330                 335
Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
            340                 345                 350
Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
        355                 360                 365
Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
    370                 375                 380
Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
385                 390                 395                 400
Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
                405                 410                 415
Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
            420                 425                 430
Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
        435                 440                 445
Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
    450                 455                 460
Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
465                 470                 475                 480
Gly Gly Ser Thr Gln Asp Cys Ser Phe Gln His Ser Pro Ile Ser Ser
                485                 490                 495
Asp Phe Ala Val Lys Ile Arg Glu Leu Ser Asp Tyr Leu Leu Gln Asp
            500                 505                 510
Tyr Pro Val Thr Val Ala Ser Asn Leu Gln Asp Glu Glu Leu Cys Gly
        515                 520                 525
```

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Gly Leu Trp Arg Leu Val Leu Ala Gln Arg Trp Met Glu Arg Leu Lys
    530                 535                 540
Thr Val Ala Gly Ser Lys Met Gln Gly Leu Leu Glu Arg Val Asn Thr
545                 550                 555                 560
Glu Ile His Phe Val Thr Lys Cys Ala Phe Gln Pro Pro Pro Ser Cys
                565                 570                 575
Leu Arg Phe Val Gln Thr Asn Ile Ser Arg Leu Leu Gln Glu Thr Ser
            580                 585                 590
Glu Gln Leu Val Ala Leu Lys Pro Trp Ile Thr Arg Gln Asn Phe Ser
        595                 600                 605
Arg Cys Leu Glu Leu Gln Cys Gln Pro Asp Ser Ser Thr Leu Pro Pro
    610                 615                 620
Pro Trp Ser Pro Arg Pro Leu Glu Ala Thr Ala Pro Thr Ala Pro
625                 630                 635


<210> 33
<211> 1986
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 33
atgacagtgc tggcgccagc ctggagccca acaacctatc tcctcctgct gctgctgctg 60
agctcgggac tcagtgggac ccaggactgc tccttccaac acagccccat ctcctccgac 120
ttcgctgtca aaatccgtga gctgtctgac tacctgcttc aagattaccc agtcaccgtg 180
gcctccaacc tgcaggacga ggagctctgc gggggcctct ggcggctggt cctggcacag 240
cgctggatgg agcggctcaa gactgtcgct gggtccaaga tgcaaggctt gctggagcgc 300
gtgaacacgg agatacactt tgtcaccaaa tgtgcctttc agcccccccc cagctgtctt 360
cgcttcgtcc agaccaacat ctcccgcctc ctgcaggaga cctccgagca gctggtggcg 420
ctgaagccct ggatcactcg ccagaacttc tcccggtgcc tggagctgca gtgtcagccc 480
gactcctcaa ccctgccacc cccatggagt ccccggcccc tggaggccac agccccgaca 540
gccccggagc ccaaatcttg tgacaaaact cacacatgcc caccgtgccc agcacctgaa 600
ctcctggggg gaccgtcagt cttcctcttc cccccaaaac ccaaggacac cctcatgatc 660
tcccggaccc ctgaggtcac atgcgtggtg gtggacgtga gccacgaaga ccctgaggtc 720
aagttcaact ggtacgtgga cggcgtggag gtgcataatg ccaagacaaa gccgcgggag 780
gagcagtaca acagcacgta ccgggtggtc tgcgtcctca ccgtcctgca ccaggactgg 840
ctgaatggca aggagtacaa gtgcaaggtc tccaacaaag ccctcccagc ccccatcgag 900
aaaaccatct ccaaagccaa agggcagccc cgagaaccac aggtgtacac cctgccccca 960
tcccgggatg agctgaccaa gaaccaggtc agcctgacct gcctggtcaa aggcttctat 1020
cccagcgaca tcgccgtgga gtgggagagc aatgggcagc cggagaacaa ctacaagacc 1080
acgcctcccg tgctggactc cgacggctcc ttcttcctct acagcaagct caccgtggac 1140
aagagcaggt ggcagcaggg gaacgtcttc tcatgctccg tgatgcatga ggctctgcac 1200
aaccactaca cgcagaagag cctctccctg tctcccggta aagaggtcca gctgcagcag 1260
tctggacctg agctggtaaa gcctggggct tcagtgaaga tgtcctgcaa ggcttctgga 1320
tacacattca ctagctatgt tatgcactgg gtgaagcaga agcctgggca gggccttgac 1380
tggattggat atattgttcc ttacaatgat ggcactaagt acaatgagaa gttcaaaggc 1440
aaggccacac tgacttcaga caaatcctcc agcacagcct acatggagct cagcagactg 1500
acctctgagg actctgcggt ctattattgt gtctacggta gtaggtacga ctggtattta 1560
gatgtctggg gcgcagggac cacggtcacc gtctcctcag gcggtggagg ctctggtgga 1620
ggcggttcag gaggcggtgg atctaacatt atgatgacac agtcgccatc atctctggct 1680
gtgtctgcag gagaaaaggt cactatgagc tgtaagtcca gtcaaagtgt tttatacagt 1740
tcaaatcaga agaactactt ggcctggtac cagcagaaac cagggcagtc tcctaaactg 1800
ctgatctact gggcatccac tagggaatct ggtgtccctg atcgcttcac aggcagtgga 1860
tctgggacag attttactct taccatcagc agtgtacaag ctgaagacct ggcagtttat 1920
```

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tactgtcatc aatatttctc ctcatacacg ttcggagggg ggaccaagct ggaaataaag 1980
cggtga                                                            1986

<210> 34
<211> 661
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 34
Met Thr Val Leu Ala Pro Ala Trp Ser Pro Thr Thr Tyr Leu Leu Leu
 1               5                  10                  15
Leu Leu Leu Leu Ser Ser Gly Leu Ser Gly Thr Gln Asp Cys Ser Phe
            20                  25                  30
Gln His Ser Pro Ile Ser Ser Asp Phe Ala Val Lys Ile Arg Glu Leu
        35                  40                  45
Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val Thr Val Ala Ser Asn Leu
    50                  55                  60

Gln Asp Glu Glu Leu Cys Gly Gly Leu Trp Arg Leu Val Leu Ala Gln
65                  70                  75                  80
Arg Trp Met Glu Arg Leu Lys Thr Val Ala Gly Ser Lys Met Gln Gly
                85                  90                  95
Leu Leu Glu Arg Val Asn Thr Glu Ile His Phe Val Thr Lys Cys Ala
            100                 105                 110
Phe Gln Pro Pro Pro Ser Cys Leu Arg Phe Val Gln Thr Asn Ile Ser
        115                 120                 125
Arg Leu Leu Gln Glu Thr Ser Glu Gln Leu Val Ala Leu Lys Pro Trp
    130                 135                 140
Ile Thr Arg Gln Asn Phe Ser Arg Cys Leu Glu Leu Gln Cys Gln Pro
145                 150                 155                 160
Asp Ser Ser Thr Leu Pro Pro Pro Trp Ser Pro Arg Pro Leu Glu Ala
                165                 170                 175
Thr Ala Pro Thr Ala Pro Glu Pro Lys Ser Cys Asp Lys Thr His Thr
            180                 185                 190
Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe
        195                 200                 205
Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
    210                 215                 220
Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
225                 230                 235                 240
Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
                245                 250                 255
Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
            260                 265                 270
Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
        275                 280                 285
Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
    290                 295                 300
Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
305                 310                 315                 320
Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
                325                 330                 335
Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
            340                 345                 350
```

```
Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
        355                 360                 365
Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
    370                 375                 380
Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
385                 390                 395                 400
Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Glu Val

                405                 410                 415
Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala Ser Val
            420                 425                 430
Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr Val Met
        435                 440                 445
His Trp Val Lys Gln Lys Pro Gly Gln Gly Leu Asp Trp Ile Gly Tyr
    450                 455                 460
Ile Val Pro Tyr Asn Asp Gly Thr Lys Tyr Asn Glu Lys Phe Lys Gly
465                 470                 475                 480
Lys Ala Thr Leu Thr Ser Asp Lys Ser Ser Ser Thr Ala Tyr Met Glu
                485                 490                 495
Leu Ser Arg Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Val Tyr
            500                 505                 510
Gly Ser Arg Tyr Asp Trp Tyr Leu Asp Val Trp Gly Ala Gly Thr Thr
        515                 520                 525
Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
    530                 535                 540
Gly Gly Gly Ser Asn Ile Met Met Thr Gln Ser Pro Ser Ser Leu Ala
545                 550                 555                 560
Val Ser Ala Gly Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser
                565                 570                 575
Val Leu Tyr Ser Ser Asn Gln Lys Asn Tyr Leu Ala Trp Tyr Gln Gln
            580                 585                 590
Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg
        595                 600                 605
Glu Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp
    610                 615                 620
Phe Thr Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Val Tyr
625                 630                 635                 640
Tyr Cys His Gln Tyr Phe Ser Ser Tyr Thr Phe Gly Gly Gly Thr Lys
                645                 650                 655
Leu Glu Ile Lys Arg
            660


<210> 35
<211> 426
<212> DNA
<213> Mus musculus

<400> 35
gccaccatgg gattcagcag gatctttctc ttcctcctgt cagtaactac aggtgtccac 60
tcccaggtac aactacagca gcctggggct gagctggtga agcctggggc ctcagtgaag 120
atgtcctgca aggcttctgg ctacacattt accagttaca atatgcactg ggtaaagcag 180
acacctggtc ggggcctgga atggattgga gctatttatc caggaaatgg tgatacttcc 240
tacaatcaga agttcaaggg caaggccaca ctgactgcag acaaatcctc cagcacagcc 300
tacatgcagc tcagcagcct gacatctgaa gactctgcgg tctattactg tgcaagatcg 360
acttactacg gcggtgactg gtacttcaat gtctggggcg cagggaccac ggtcaccgtc 420
tctgca                                                            426
```

```
<210> 36
<211> 140
<212> PRT
<213> Mus musculus

<400> 36
Met Gly Phe Ser Arg Ile Phe Leu Phe Leu Leu Ser Val Thr Thr Gly
 1               5                  10                  15
Val His Ser Gln Val Gln Leu Gln Gln Pro Gly Ala Glu Leu Val Lys
            20                  25                  30
Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe
        35                  40                  45
Thr Ser Tyr Asn Met His Trp Val Lys Gln Thr Pro Gly Arg Gly Leu
    50                  55                  60
Glu Trp Ile Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn
65                  70                  75                  80
Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser
                85                  90                  95
Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val
            100                 105                 110
Tyr Tyr Cys Ala Arg Ser Thr Tyr Tyr Gly Gly Asp Trp Tyr Phe Asn
        115                 120                 125
Val Trp Gly Ala Gly Thr Thr Val Thr Val Ser Ala
    130                 135                 140


<210> 37
<211> 390
<212> DNA
<213> Mus musculus

<400> 37
accatggatt ttcaagtgca gattttcagc ttcctgctaa tcagtgcttc agtcataatg 60
tccagaggac aaattgttct ctcccagtct ccagcaatcc tgtctgcatc tccaggggag 120
aaggtcacaa tgacttgcag ggccagctca agtgtaagtt acatccactg gttccagcag 180
aagccaggat cctcccccaa accctggatt tatgccacat ccaacctggc ttctggagtc 240
cctgttcgct tcagtggcag tgggtctggg acctcttact ctctcacaat cagtagagtg 300
gaggctgaag atgctgccac ttattactgc cagcagtgga ctagtaaccc acccacgttc 360
ggtggtggga ccaagctgga gatcaaacga                                  390

<210> 38
<211> 129
<212> PRT
<213> Mus musculus

<400> 38
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1               5                  10                  15
Val Ile Met Ser Arg Gly Gln Ile Val Leu Ser Gln Ser Pro Ala Ile
            20                  25                  30
Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser
        35                  40                  45
Ser Ser Val Ser Tyr Ile His Trp Phe Gln Gln Lys Pro Gly Ser Ser
    50                  55                  60
Pro Lys Pro Trp Ile Tyr Ala Thr Ser Asn Leu Ala Ser Gly Val Pro
65                  70                  75                  80
```

```
Val Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
                85                  90                  95
Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp
            100                 105                 110
Thr Ser Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
        115                 120                 125
Arg
```

<210> 39
<211> 2021
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 39
gccaccatgg gattcagcag gatctttctc ttcctcctgt cagtaactac aggtgtccac 60
tcccaggtac aactacagca gcctggggct gagctggtga agcctggggc ctcagtgaag 120
atgtcctgca aggcttctgg ctacacattt accagttaca atatgcactg ggtaaagcag 180
acacctggtc ggggcctgga atggattgga gctatttatc caggaaatgg tgatacttcc 240
tacaatcaga agttcaaggg caaggccaca ctgactgcag acaaatcctc cagcacagcc 300
tacatgcagc tcagcagcct gacatctgaa gactctgcgg tctattactg tgcaagatcg 360
acttactacg gcggtgactg gtacttcaat gtctggggcg cagggaccac ggtcaccgtc 420
tctgcagcta gcaccaaggg cccatcggtc ttccccctgg caccctcctc caagagcacc 480
tctgggggca cagcggccct gggctgcctg gtcaaggact acttccccga accggtgacg 540
gtgtcttgga actcaggcgc cctgaccagc ggcgtgcaca ccttcccggc tgtcctacag 600
tcctcaggac tctactccct cagcagcgtg gtgaccgtgc cctccagcag cttgggcacc 660
cagacctaca tctgcaacgt gaatcacaag cccagcaaca ccaaggtgga caagaaagtt 720
ggtgagaggc cagcacaggg agggagggtg tctgctggaa gcaggctcag cgctcctgcc 780
tggacgcatc ccggctatgc agccccagtc cagggcagca aggcaggccc cgtctgcctc 840
ttcacccgga gcctctgccc gccccactca tgctcaggga gagggtcttc tggctttttc 900
ccaggctctg ggcaggcaca ggctaggtgc ccctaaccca ggccctgcac acaaaggggc 960
aggtgctggg ctcagacctg ccaagagcca tatccgggag gaccctgccc ctgacctaag 1020
cccaccccaa aggccaaact ctccactccc tcagctcgga caccttctct cctcccagat 1080
tccagtaact cccaatcttc tctctgcaga gcccaaatct tgtgacaaaa ctcacacatg 1140
cccaccgtgc ccaggtaagc cagcccaggc ctcgccctcc agctcaaggc gggacaggtg 1200
ccctagagta gcctgcatcc agggacaggc cccagccggg tgctgacacg tccacctcca 1260
tctcttcctc agcacctgaa ctcctggggg gaccgtcagt cttcctcttc cccccaaaac 1320
ccaaggacac cctcatgatc tcccggaccc ctgaggtcac atgcgtggtg gtggacgtga 1380
gccacgaaga ccctgaggtc aagttcaact ggtacgtgga cggcgtggag gtgcataatg 1440
ccaagacaaa gccgcgggag gagcagtaca acagcacgta ccgggtggtc tgcgtcctca 1500
ccgtcctgca ccaggactgg ctgaatggca aggagtacaa gtgcaaggtc tccaacaaag 1560
ccctcccagc ccccatcgag aaaaccatct ccaaagccaa aggtgggacc cgtggggtgc 1620
gagggccaca tggacagagg ccggctcggc ccaccctctg ccctgagagt gaccgctgta 1680
ccaacctctg tcctacaggg cagccccgag aaccacaggt gtacaccctg cccccatccc 1740
gggatgagct gaccaagaac caggtcagcc tgacctgcct ggtcaaaggc ttctatccca 1800
gcgacatcgc cgtggagtgg gagagcaatg ggcagccgga gaacaactac aagaccacgc 1860
ctcccgtgct ggactccgac ggctccttct tcctctacag caagctcacc gtggacaaga 1920
gcaggtggca gcaggggaac gtcttctcat gctccgtgat gcatgaggct ctgcacaacc 1980
actacacgca gaagagcctc tccctgtctc ccggtaaatg a 2021

<210> 40
<211> 470
<212> PRT

```
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 40
Met Gly Phe Ser Arg Ile Phe Leu Phe Leu Leu Ser Val Thr Thr Gly
 1               5                  10                  15
Val His Ser Gln Val Gln Leu Gln Gln Pro Gly Ala Glu Leu Val Lys
            20                  25                  30
Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe
        35                  40                  45
Thr Ser Tyr Asn Met His Trp Val Lys Gln Thr Pro Gly Arg Gly Leu
    50                  55                  60
Glu Trp Ile Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn
65                  70                  75                  80
Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser
                85                  90                  95
Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val
            100                 105                 110
Tyr Tyr Cys Ala Arg Ser Thr Tyr Tyr Gly Gly Asp Trp Tyr Phe Asn
        115                 120                 125
Val Trp Gly Ala Gly Thr Thr Val Thr Val Ser Ala Ala Ser Thr Lys
    130                 135                 140
Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly
145                 150                 155                 160
Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro
                165                 170                 175
Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr
            180                 185                 190
Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val
        195                 200                 205
Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn
    210                 215                 220
Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro
225                 230                 235                 240
Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
                245                 250                 255
Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
            260                 265                 270
Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
        275                 280                 285
Val Ser His Glu Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Asp Gly
    290                 295                 300
Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
305                 310                 315                 320
Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
                325                 330                 335
Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro
            340                 345                 350
Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
        355                 360                 365
Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn
    370                 375                 380
Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
385                 390                 395                 400
Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
```

```
                405                 410                 415
Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
            420                 425                 430
Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
        435                 440                 445
Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
    450                 455                 460
Ser Leu Ser Pro Gly Lys
465                 470
```

```
<210> 41
<211> 711

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 41
accatggatt ttcaagtgca gattttcagc ttcctgctaa tcagtgcttc agtcataatg 60
tccagaggac aaattgttct ctcccagtct ccagcaatcc tgtctgcatc tccaggggag 120
aaggtcacaa tgacttgcag ggccagctca agtgtaagtt acatccactg gttccagcag 180
aagccaggat cctcccccaa accctggatt tatgccacat ccaacctggc ttctggagtc 240
cctgttcgct tcagtggcag tgggtctggg acctcttact ctctcacaat cagtagagtg 300
gaggctgaag atgctgccac ttattactgc cagcagtgga ctagtaaccc acccacgttc 360

ggtggtggga ccaagctgga gatcaaacga actgtggctg caccatctgt cttcatcttc 420
ccgccatctg atgagcagtt gaaatctgga actgcctctg ttgtgtgcct gctgaataac 480
ttctatccca gagaggccaa agtacagtgg aaggtggata acgccctcca atcgggtaac 540
tcccaggaga gtgtcacaga gcaggacagc aaggacagca cctacagcct cagcagcacc 600
ctgacgctga gcaaagcaga ctacgagaaa cacaaagtct acgcctgcga agtcacccat 660
cagggcctga gctcgcccgt cacaaagagc ttcaacaggg gagagtgtta g          711

<210> 42
<211> 235
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 42
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1               5                  10                  15
Val Ile Met Ser Arg Gly Gln Ile Val Leu Ser Gln Ser Pro Ala Ile
            20                  25                  30
Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser
        35                  40                  45
Ser Ser Val Ser Tyr Ile His Trp Phe Gln Gln Lys Pro Gly Ser Ser
    50                  55                  60
Pro Lys Pro Trp Ile Tyr Ala Thr Ser Asn Leu Ala Ser Gly Val Pro
65                  70                  75                  80
Val Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
                85                  90                  95
Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp
```

```
            100                 105                 110
Thr Ser Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
    115                 120                 125
Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
    130                 135                 140
Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
145                 150                 155                 160
Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
                165                 170                 175
Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
            180                 185                 190
Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
        195                 200                 205
Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser

    210                 215                 220
Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225                 230                 235
```

<210> 43
<211> 2489
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 43

```
gccaccatgg gattcagcag gatctttctc ttcctcctgt cagtaactac aggtgtccac 60
tcccaggtac aactacagca gcctggggct gagctggtga agcctggggc ctcagtgaag 120
atgtcctgca aggcttctgg ctacacattt accagttaca atatgcactg ggtaaagcag 180
acacctggtc ggggcctgga atggattgga gctatttatc caggaaatgg tgatacttcc 240
tacaatcaga agttcaaggg caaggccaca ctgactgcag acaaatcctc cagcacagcc 300
tacatgcagc tcagcagcct gacatctgaa gactctgcgg tctattactg tgcaagatcg 360
acttactacg gcggtgactg gtacttcaat gtctggggcg cagggaccac ggtcaccgtc 420
tctgcagcta gcaccaaggg cccatcggtc ttccccctgg caccctcctc caagagcacc 480
tctgggggca cagcggccct gggctgcctg gtcaaggact acttccccga accggtgacg 540
gtgtcttgga actcaggcgc cctgaccagc ggcgtgcaca ccttcccggc tgtcctacag 600
tcctcaggac tctactccct cagcagcgtg gtgaccgtgc cctccagcag cttgggcacc 660
cagacctaca tctgcaacgt gaatcacaag cccagcaaca ccaaggtgga caagaaagtt 720
ggtgagaggc cagcacaggg agggagggtg tctgctggaa gcaggctcag cgctcctgcc 780
tggacgcatc ccggctatgc agccccagtc cagggcagca aggcaggccc cgtctgcctc 840
ttcacccgga gcctctgccc gccccactca tgctcaggga gagggtcttc tggctttttc 900
ccaggctctg ggcaggcaca ggctaggtgc ccctaaccca ggccctgcac acaaaggggc 960
aggtgctggg ctcagacctg ccaagagcca tatccgggag gaccctgccc ctgacctaag 1020
cccaccccaa aggccaaact ctccactccc tcagctcgga caccttctct cctcccagat 1080
tccagtaact cccaatcttc tctctgcaga gcccaaatct tgtgacaaaa ctcacacatg 1140
cccaccgtgc ccaggtaagc cagcccaggc ctcgccctcc agctcaaggc gggacaggtg 1200
ccctagagta gcctgcatcc agggacaggc cccagccggg tgctgacacg tccacctcca 1260
tctcttcctc agcacctgaa ctcctggggg gaccgtcagt cttcctcttc cccccaaaac 1320
ccaaggacac cctcatgatc tcccggaccc ctgaggtcac atgcgtggtg gtggacgtga 1380
gccacgaaga ccctgaggtc aagttcaact ggtacgtgga cggcgtggag gtgcataatg 1440
ccaagacaaa gccgcgggag gagcagtaca acagcacgta ccgggtggtc tgcgtcctca 1500
ccgtcctgca ccaggactgg ctgaatggca aggagtacaa gtgcaaggtc tccaacaaag 1560
ccctcccagc ccccatcgag aaaaccatct ccaaagccaa aggtgggacc cgtggggtgc 1620
gagggccaca tggacagagg ccggctcggc ccaccctctg ccctgagagt gaccgctgta 1680
```

```
ccaacctctg tcctacaggg cagccccgag aaccacaggt gtacaccctg cccccatccc 1740
gggatgagct gaccaagaac caggtcagcc tgacctgcct ggtcaaaggc ttctatccca 1800
gcgacatcgc cgtggagtgg gagagcaatg ggcagccgga gaacaactac aagaccacgc 1860
ctcccgtgct ggactccgac ggctccttct tcctctacag caagctcacc gtggacaaga 1920
gcaggtggca gcaggggaac gtcttctcat gctccgtgat gcatgaggct ctgcacaacc 1980
actacacgca gaagagcctc tccctgtctc ccggtaaaac ccaggactgc tccttccaac 2040
acagccccat ctcctccgac ttcgctgtca aaatccgtga gctgtctgac tacctgcttc 2100
aagattaccc agtcaccgtg gcctccaacc tgcaggacga ggagctctgc gggggcctct 2160
ggcggctggt cctggcacag cgctggatgg agcggctcaa gactgtcgct gggtccaaga 2220
tgcaaggctt gctggagcgc gtgaacacgg agatacactt tgtcaccaaa tgtgcctttc 2280
agcccccccc cagctgtctt cgcttcgtcc agaccaacat ctcccgcctc ctgcaggaga 2340
cctccgagca gctggtggcg ctgaagccct ggatcactcg ccagaacttc tcccggtgcc 2400
tggagctgca gtgtcagccc gactcctcaa ccctgccacc cccatggagt ccccggcccc 2460
tggaggccac agccccgaca gccccgtga                                   2489

<210> 44
<211> 626
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 44
Met Gly Phe Ser Arg Ile Phe Leu Phe Leu Leu Ser Val Thr Thr Gly
 1              5                   10                  15
Val His Ser Gln Val Gln Leu Gln Gln Pro Gly Ala Glu Leu Val Lys
            20                  25                  30
Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe
        35                  40                  45
Thr Ser Tyr Asn Met His Trp Val Lys Gln Thr Pro Gly Arg Gly Leu
    50                  55                  60
Glu Trp Ile Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn
65                  70                  75                  80
Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser
                85                  90                  95
Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val
            100                 105                 110
Tyr Tyr Cys Ala Arg Ser Thr Tyr Tyr Gly Gly Asp Trp Tyr Phe Asn
        115                 120                 125
Val Trp Gly Ala Gly Thr Thr Val Thr Val Ser Ala Ala Ser Thr Lys
    130                 135                 140
Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly
145                 150                 155                 160
Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro
                165                 170                 175
Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr
            180                 185                 190
Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val
        195                 200                 205
Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn
    210                 215                 220
Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro
225                 230                 235                 240
Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
                245                 250                 255
Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
```

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            260                 265                 270
Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
        275                 280                 285
Val Ser His Glu Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Asp Gly
    290                 295                 300
Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
305                 310                 315                 320
Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
                325                 330                 335
Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro
            340                 345                 350
Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
        355                 360                 365

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn
    370                 375                 380
Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
385                 390                 395                 400
Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
                405                 410                 415
Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
            420                 425                 430
Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
        435                 440                 445
Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
    450                 455                 460
Ser Leu Ser Pro Gly Lys Thr Gln Asp Cys Ser Phe Gln His Ser Pro
465                 470                 475                 480
Ile Ser Ser Asp Phe Ala Val Lys Ile Arg Glu Leu Ser Asp Tyr Leu
                485                 490                 495
Leu Gln Asp Tyr Pro Val Thr Val Ala Ser Asn Leu Gln Asp Glu Glu
            500                 505                 510
Leu Cys Gly Gly Leu Trp Arg Leu Val Leu Ala Gln Arg Trp Met Glu
        515                 520                 525
Arg Leu Lys Thr Val Ala Gly Ser Lys Met Gln Gly Leu Leu Glu Arg
    530                 535                 540
Val Asn Thr Glu Ile His Phe Val Thr Lys Cys Ala Phe Gln Pro Pro
545                 550                 555                 560
Pro Ser Cys Leu Arg Phe Val Gln Thr Asn Ile Ser Arg Leu Leu Gln
                565                 570                 575
Glu Thr Ser Glu Gln Leu Val Ala Leu Lys Pro Trp Ile Thr Arg Gln
            580                 585                 590
Asn Phe Ser Arg Cys Leu Glu Leu Gln Cys Gln Pro Asp Ser Ser Thr
        595                 600                 605
Leu Pro Pro Pro Trp Ser Pro Arg Pro Leu Glu Ala Thr Ala Pro Thr
    610                 615                 620
Ala Pro
625


<210> 45
<211> 2534
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct
```

<400> 45
gccaccatgg gattcagcag gatctttctc ttcctcctgt cagtaactac aggtgtccac 60
tcccaggtac aactacagca gcctggggct gagctggtga agcctggggc ctcagtgaag 120
atgtcctgca aggcttctgg ctacacattt accagttaca atatgcactg ggtaaagcag 180
acacctggtc ggggcctgga atggattgga gctatttatc caggaaatgg tgatacttcc 240
tacaatcaga agttcaaggg caaggccaca ctgactgcag acaaatcctc cagcacagcc 300
tacatgcagc tcagcagcct gacatctgaa gactctgcgg tctattactg tgcaagatcg 360
acttactacg gcggtgactg gtacttcaat gtctggggcg cagggaccac ggtcaccgtc 420
tctgcagcta gcaccaaggg cccatcggtc ttccccctgg caccctcctc caagagcacc 480
tctgggggca cagcggccct gggctgcctg gtcaaggact acttccccga accggtgacg 540
gtgtcttgga actcaggcgc cctgaccagc ggcgtgcaca ccttcccggc tgtcctacag 600
tcctcaggac tctactccct cagcagcgtg gtgaccgtgc cctccagcag cttgggcacc 660
cagacctaca tctgcaacgt gaatcacaag cccagcaaca ccaaggtgga caagaaagtt 720
ggtgagaggc cagcacaggg agggagggtg tctgctggaa gcaggctcag cgctcctgcc 780
tggacgcatc ccggctatgc agccccagtc cagggcagca aggcaggccc cgtctgcctc 840
ttcacccgga gcctctgccc gccccactca tgctcaggga gagggtcttc tggctttttc 900
ccaggctctg ggcaggcaca ggctaggtgc ccctaaccca ggccctgcac acaaaggggc 960
aggtgctggg ctcagacctg ccaagagcca tatccgggag gaccctgccc ctgacctaag 1020
cccaccccaa aggccaaact ctccactccc tcagctcgga caccttctct cctcccagat 1080
tccagtaact cccaatcttc tctctgcaga gcccaaatct tgtgacaaaa ctcacacatg 1140
cccaccgtgc ccaggtaagc cagcccaggc ctcgccctcc agctcaaggc gggacaggtg 1200
ccctagagta gcctgcatcc agggacaggc cccagccggg tgctgacacg tccacctcca 1260
tctcttcctc agcacctgaa ctcctggggg gaccgtcagt cttcctcttc cccccaaaac 1320
ccaaggacac cctcatgatc tcccggaccc ctgaggtcac atgcgtggtg gtggacgtga 1380
gccacgaaga ccctgaggtc aagttcaact ggtacgtgga cggcgtggag gtgcataatg 1440
ccaagacaaa gccgcgggag gagcagtaca acagcacgta ccgggtggtc tgcgtcctca 1500
ccgtcctgca ccaggactgg ctgaatggca aggagtacaa gtgcaaggtc tccaacaaag 1560
ccctcccagc ccccatcgag aaaaccatct ccaaagccaa aggtgggacc cgtggggtgc 1620
gagggccaca tggacagagg ccggctcggc ccaccctctg ccctgagagt gaccgctgta 1680
ccaacctctg tcctacaggg cagccccgag aaccacaggt gtacaccctg cccccatccc 1740
gggatgagct gaccaagaac caggtcagcc tgacctgcct ggtcaaaggc ttctatccca 1800
gcgacatcgc cgtggagtgg gagagcaatg ggcagccgga gaacaactac aagaccacgc 1860
ctcccgtgct ggactccgac ggctccttct tcctctacag caagctcacc gtggacaaga 1920
gcaggtggca gcaggggaac gtcttctcat gctccgtgat gcatgaggct ctgcacaacc 1980
actacacgca gaagagcctc tccctgtctc ccggtaaagg cggtggaggc tctggtggag 2040
gcggttcagg aggcggtgga tctacccagg actgctcctt ccaacacagc cccatctcct 2100
ccgacttcgc tgtcaaaatc cgtgagctgt ctgactacct gcttcaagat tacccagtca 2160
ccgtggcctc caacctgcag gacgaggagc tctgcggggg cctctggcgg ctggtcctgg 2220
cacagcgctg gatggagcgg ctcaagactg tcgctgggtc caagatgcaa ggcttgctgg 2280
agcgcgtgaa cacggagata cactttgtca ccaaatgtgc ctttcagccc ccccccagct 2340
gtcttcgctt cgtccagacc aacatctccc gcctcctgca ggagacctcc gagcagctgg 2400
tggcgctgaa gccctggatc actcgccaga acttctcccg gtgcctggag ctgcagtgtc 2460
agcccgactc ctcaaccctg ccaccccccat ggagtccccg gcccctggag gccacagccc 2520
cgacagcccc gtga 2534

<210> 46
<211> 641
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 46
Met Gly Phe Ser Arg Ile Phe Leu Phe Leu Leu Ser Val Thr Thr Gly
1 5 10 15

```
Val His Ser Gln Val Gln Leu Gln Gln Pro Gly Ala Glu Leu Val Lys
            20                  25                  30
Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe
        35                  40                  45
Thr Ser Tyr Asn Met His Trp Val Lys Gln Thr Pro Gly Arg Gly Leu
    50                  55                  60
Glu Trp Ile Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn
65                  70                  75                  80
Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser
                85                  90                  95
Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val
            100                 105                 110
Tyr Tyr Cys Ala Arg Ser Thr Tyr Tyr Gly Gly Asp Trp Tyr Phe Asn
        115                 120                 125
Val Trp Gly Ala Gly Thr Thr Val Thr Val Ser Ala Ala Ser Thr Lys
    130                 135                 140
Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly
145                 150                 155                 160
Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro
                165                 170                 175
Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr
            180                 185                 190
Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val
        195                 200                 205
Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn
    210                 215                 220
Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro
225                 230                 235                 240
Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
                245                 250                 255
Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
            260                 265                 270
Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
        275                 280                 285
Val Ser His Glu Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Asp Gly
    290                 295                 300
Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
305                 310                 315                 320
Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
                325                 330                 335
Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro
            340                 345                 350
Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
        355                 360                 365
Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn
    370                 375                 380
Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
385                 390                 395                 400
Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
                405                 410                 415
Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
            420                 425                 430
Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
        435                 440                 445
Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
    450                 455                 460
```

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Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
465                 470                 475                 480
Gly Gly Gly Gly Ser Thr Gln Asp Cys Ser Phe Gln His Ser Pro Ile
                485                 490                 495
Ser Ser Asp Phe Ala Val Lys Ile Arg Glu Leu Ser Asp Tyr Leu Leu
            500                 505                 510
Gln Asp Tyr Pro Val Thr Val Ala Ser Asn Leu Gln Asp Glu Glu Leu
        515                 520                 525
Cys Gly Gly Leu Trp Arg Leu Val Leu Ala Gln Arg Trp Met Glu Arg
    530                 535                 540
Leu Lys Thr Val Ala Gly Ser Lys Met Gln Gly Leu Leu Glu Arg Val
545                 550                 555                 560
Asn Thr Glu Ile His Phe Val Thr Lys Cys Ala Phe Gln Pro Pro Pro
                565                 570                 575
Ser Cys Leu Arg Phe Val Gln Thr Asn Ile Ser Arg Leu Leu Gln Glu
            580                 585                 590
Thr Ser Glu Gln Leu Val Ala Leu Lys Pro Trp Ile Thr Arg Gln Asn
        595                 600                 605
Phe Ser Arg Cys Leu Glu Leu Gln Cys Gln Pro Asp Ser Ser Thr Leu
    610                 615                 620
Pro Pro Pro Trp Ser Pro Arg Pro Leu Glu Ala Thr Ala Pro Thr Ala
625                 630                 635                 640
Pro


<210> 47
<211> 1974
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 47
atgacagtgc tggcgccagc ctggagccca acaacctatc tcctcctgct gctgctgctg 60
agctcgggac tcagtgggac ccaggactgc tccttccaac acagccccat ctcctccgac 120
ttcgctgtca aaatccgtga gctgtctgac tacctgcttc aagattaccc agtcaccgtg 180
gcctccaacc tgcaggacga ggagctctgc gggggcctct ggcggctggt cctggcacag 240
cgctggatgg agcggctcaa gactgtcgct gggtccaaga tgcaaggctt gctggagcgc 300
gtgaacacgg agatacactt tgtcaccaaa tgtgcctttc agcccccccc cagctgtctt 360
cgcttcgtcc agaccaacat ctcccgcctc ctgcaggaga cctccgagca gctggtggcg 420
ctgaagccct ggatcactcg ccagaacttc tcccggtgcc tggagctgca gtgtcagccc 480
gactcctcaa ccctgccacc cccatggagt ccccggcccc tggaggccac agccccgaca 540
gccccggagc ccaaatcttg tgacaaaact cacacatgcc caccgtgccc agcacctgaa 600
ctcctggggg gaccgtcagt cttcctcttc cccccaaaac ccaaggacac cctcatgatc 660
tcccggaccc ctgaggtcac atgcgtggtg gtggacgtga gccacgaaga ccctgaggtc 720
aagttcaact ggtacgtgga cggcgtggag gtgcataatg ccaagacaaa gccgcgggag 780
gagcagtaca acagcacgta ccgggtggtc tgcgtcctca ccgtcctgca ccaggactgg 840
ctgaatggca aggagtacaa gtgcaaggtc tccaacaaag ccctcccagc ccccatcgag 900
aaaaccatct ccaaagccaa agggcagccc cgagaaccac aggtgtacac cctgccccca 960
tcccgggatg agctgaccaa gaaccaggtc agcctgacct gcctggtcaa aggcttctat 1020
cccagcgaca tcgccgtgga gtgggagagc aatgggcagc cggagaacaa ctacaagacc 1080
acgcctcccg tgctggactc cgacggctcc ttcttcctct acagcaagct caccgtggac 1140
aagagcaggt ggcagcaggg gaacgtcttc tcatgctccg tgatgcatga ggctctgcac 1200
aaccactaca cgcagaagag cctctccctg tctcccggta aacaggtaca actacagcag 1260
cctggggctg agctggtgaa gcctggggcc tcagtgaaga tgtcctgcaa ggcttctggc 1320
```

```
tacacattta ccagttacaa tatgcactgg gtaaagcaga cacctggtcg gggcctggaa 1380
tggattggag ctatttatcc aggaaatggt gatacttcct acaatcagaa gttcaagggc 1440
aaggccacac tgactgcaga caaatcctcc agcacagcct acatgcagct cagcagcctg 1500
acatctgaag actctgcggt ctattactgt gcaagatcga cttactacgg cggtgactgg 1560
tacttcaatg tctggggcgc agggaccacg gtcaccgtct ctgcaggcgg tggaggctct 1620
ggtggaggcg gttcaggagg cggtggatct caaattgttc tctcccagtc tccagcaatc 1680
ctgtctgcat ctccagggga gaaggtcaca atgacttgca gggccagctc aagtgtaagt 1740
tacatccact ggttccagca gaagccagga tcctccccca aaccctggat ttatgccaca 1800
tccaacctgg cttctggagt ccctgttcgc ttcagtggca gtgggtctgg gacctcttac 1860
tctctcacaa tcagtagagt ggaggctgaa gatgctgcca cttattactg ccagcagtgg 1920
actagtaacc cacccacgtt cggtggtggg accaagctgg agatcaaacg atga       1974

<210> 48
<211> 657
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 48
Met Thr Val Leu Ala Pro Ala Trp Ser Pro Thr Thr Tyr Leu Leu Leu
 1               5                  10                  15
Leu Leu Leu Leu Ser Ser Gly Leu Ser Gly Thr Gln Asp Cys Ser Phe
            20                  25                  30
Gln His Ser Pro Ile Ser Ser Asp Phe Ala Val Lys Ile Arg Glu Leu
        35                  40                  45
Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val Thr Val Ala Ser Asn Leu
    50                  55                  60
Gln Asp Glu Glu Leu Cys Gly Gly Leu Trp Arg Leu Val Leu Ala Gln
65                  70                  75                  80
Arg Trp Met Glu Arg Leu Lys Thr Val Ala Gly Ser Lys Met Gln Gly
                85                  90                  95
Leu Leu Glu Arg Val Asn Thr Glu Ile His Phe Val Thr Lys Cys Ala
            100                 105                 110
Phe Gln Pro Pro Pro Ser Cys Leu Arg Phe Val Gln Thr Asn Ile Ser
        115                 120                 125
Arg Leu Leu Gln Glu Thr Ser Glu Gln Leu Val Ala Leu Lys Pro Trp
    130                 135                 140
Ile Thr Arg Gln Asn Phe Ser Arg Cys Leu Glu Leu Gln Cys Gln Pro
145                 150                 155                 160
Asp Ser Ser Thr Leu Pro Pro Pro Trp Ser Pro Arg Pro Leu Glu Ala
                165                 170                 175
Thr Ala Pro Thr Ala Pro Glu Pro Lys Ser Cys Asp Lys Thr His Thr
            180                 185                 190
Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe
        195                 200                 205
Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
    210                 215                 220
Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
225                 230                 235                 240
Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
                245                 250                 255
Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
            260                 265                 270
Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
        275                 280                 285
```

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Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
    290                 295                 300
Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
305                 310                 315                 320
Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
                325                 330                 335
Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
            340                 345                 350
Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
        355                 360                 365
Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
    370                 375                 380
Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
385                 390                 395                 400
Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Gln Val
                405                 410                 415
Gln Leu Gln Gln Pro Gly Ala Glu Leu Val Lys Pro Gly Ala Ser Val
            420                 425                 430
Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr Asn Met
        435                 440                 445
His Trp Val Lys Gln Thr Pro Gly Arg Gly Leu Glu Trp Ile Gly Ala
    450                 455                 460
Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe Lys Gly
465                 470                 475                 480
Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr Met Gln
                485                 490                 495
Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala Arg
            500                 505                 510
Ser Thr Tyr Tyr Gly Gly Asp Trp Tyr Phe Asn Val Trp Gly Ala Gly
        515                 520                 525
Thr Thr Val Thr Val Ser Ala Gly Gly Gly Gly Ser Gly Gly Gly Gly
    530                 535                 540
Ser Gly Gly Gly Gly Ser Gln Ile Val Leu Ser Gln Ser Pro Ala Ile
545                 550                 555                 560
Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser
                565                 570                 575
Ser Ser Val Ser Tyr Ile His Trp Phe Gln Gln Lys Pro Gly Ser Ser
            580                 585                 590
Pro Lys Pro Trp Ile Tyr Ala Thr Ser Asn Leu Ala Ser Gly Val Pro
        595                 600                 605
Val Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
    610                 615                 620
Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp
625                 630                 635                 640
Thr Ser Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
                645                 650                 655
Arg
```

<210> 49
<211> 426
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

```
<400> 49
atggattttc aggtgcagat tttcagcttc ctgctaatca gtgcctcagt cataatatcc 60
agaggagagg ttcagctggt ggagtctggc ggtggcctgg tgcagccagg gggctcactc 120
cgtttgtcct gtgcagcttc tggcttcaac attaaagaca cctatataca ctgggtgcgt 180
caggccccgg gtaagggcct ggaatgggtt gcaaggattt atcctacgaa tggttatact 240
agatatgccg atagcgtcaa gggccgtttc actataagcg cagacacatc caaaaacaca 300
gcctacctgc agatgaacag cctgcgtgct gaggacactg ccgtctatta ttgttctaga 360
tggggagggg acggcttcta tgctatggac tactggggtc aaggaaccct ggtcaccgtc 420
tcctcg                                                            426

<210> 50
<211> 142
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 50
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1               5                  10                  15
Val Ile Ile Ser Arg Gly Glu Val Gln Leu Val Glu Ser Gly Gly Gly
            20                  25                  30
Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly
        35                  40                  45
Phe Asn Ile Lys Asp Thr Tyr Ile His Trp Val Arg Gln Ala Pro Gly
    50                  55                  60
Lys Gly Leu Glu Trp Val Ala Arg Ile Tyr Pro Thr Asn Gly Tyr Thr
65                  70                  75                  80
Arg Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Ala Asp Thr
                85                  90                  95
Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp
            100                 105                 110
Thr Ala Val Tyr Tyr Cys Ser Arg Trp Gly Gly Asp Gly Phe Tyr Ala
        115                 120                 125
Met Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
    130                 135                 140


<210> 51
<211> 390
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 51
atggattttc aggtgcagat tttcagcttc ctgctaatca gtgcctcagt cataatatcc 60
agaggagaca tccagatgac ccagtccccg agctccctgt ccgcctctgt gggcgatagg 120
gttaccatca cctgccgtgc cagtcaggat gtgaatactg ctgtagcctg gtatcaacag 180
aaaccaggaa aagctccgaa actactgatt tactcggcat ccttcctcta ctctggagtc 240
ccttctcgct tctctggctc cagatctggg acggatttca ctctgaccat cagcagtctg 300
cagccggaag acttcgcaac ttattactgt cagcaacatt atactactcc tcccacgttc 360
ggacagggta ccaaggtgga gatcaaacgt                                  390
```

<210> 52
<211> 130
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 52

```
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1               5                  10                  15
Val Ile Ile Ser Arg Gly Asp Ile Gln Met Thr Gln Ser Pro Ser Ser
            20                  25                  30
Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser
        35                  40                  45
Gln Asp Val Asn Thr Ala Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys

    50                  55                  60
Ala Pro Lys Leu Leu Ile Tyr Ser Ala Ser Phe Leu Tyr Ser Gly Val
65                  70                  75                  80
Pro Ser Arg Phe Ser Gly Ser Arg Ser Gly Thr Asp Phe Thr Leu Thr
                85                  90                  95
Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln
            100                 105                 110
His Tyr Thr Thr Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
        115                 120                 125
Lys Arg
    130
```

<210> 53
<211> 2021
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 53

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atggatttc aggtgcagat tttcagcttc ctgctaatca gtgcctcagt cataatatcc 60
agaggagagg ttcagctggt ggagtctggc ggtggcctgg tgcagccagg gggctcactc 120
cgtttgtcct gtgcagcttc tggcttcaac attaaagaca cctatataca ctgggtgcgt 180
caggccccgg gtaagggcct ggaatgggtt gcaaggattt atcctacgaa tggttatact 240
agatatgccg atagcgtcaa gggccgtttc actataagcg cagacacatc caaaaacaca 300
gcctacctgc agatgaacag cctgcgtgct gaggacactg ccgtctatta ttgttctaga 360
tggggagggg acggcttcta tgctatggac tactggggtc aaggaaccct ggtcaccgtc 420
tcctcggcta gcaccaaggg cccatcggtc ttccccctgg caccctcctc caagagcacc 480
tctgggggca cagcggccct gggctgcctg gtcaaggact acttccccga accggtgacg 540
gtgtcttgga actcaggcgc cctgaccagc ggcgtgcaca ccttcccggc tgtcctacag 600
tcctcaggac tctactccct cagcagcgtg gtgaccgtgc cctccagcag cttgggcacc 660
cagacctaca tctgcaacgt gaatcacaag cccagcaaca ccaaggtgga caagaaagtt 720
ggtgagaggc cagcacaggg agggagggtg tctgctggaa gcaggctcag cgctcctgcc 780
tggacgcatc ccggctatgc agccccagtc cagggcagca aggcaggccc cgtctgcctc 840
ttcacccgga gcctctgccc gccccactca tgctcaggga gagggtcttc tggctttttc 900
ccaggctctg ggcaggcaca ggctaggtgc ccctaaccca ggccctgcac acaaaggggc 960
aggtgctggg ctcagacctg ccaagagcca tatccgggag gaccctgccc ctgacctaag 1020
cccaccccaa aggccaaact ctccactccc tcagctcgga caccttctct cctcccagat 1080
```

```
tccagtaact cccaatcttc tctctgcaga gcccaaatct tgtgacaaaa ctcacacatg 1140
cccaccgtgc ccaggtaagc cagcccaggc ctcgccctcc agctcaaggc gggacaggtg 1200
ccctagagta gcctgcatcc agggacaggc cccagccggg tgctgacacg tccacctcca 1260
tctcttcctc agcacctgaa ctcctggggg gaccgtcagt cttcctcttc cccccaaaac 1320
ccaaggacac cctcatgatc tcccggaccc ctgaggtcac atgcgtggtg gtggacgtga 1380
gccacgaaga ccctgaggtc aagttcaact ggtacgtgga cggcgtggag gtgcataatg 1440
ccaagacaaa gccgcgggag gagcagtaca acagcacgta ccgggtggtc tgcgtcctca 1500
ccgtcctgca ccaggactgg ctgaatggca aggagtacaa gtgcaaggtc tccaacaaag 1560
ccctcccagc ccccatcgag aaaaccatct ccaaagccaa aggtgggacc cgtggggtgc 1620
gagggccaca tggacagagg ccggctcggc ccaccctctg ccctgagagt gaccgctgta 1680
ccaacctctg tcctacaggg cagccccgag aaccacaggt gtacaccctg cccccatccc 1740
gggatgagct gaccaagaac caggtcagcc tgacctgcct ggtcaaaggc ttctatccca 1800
gcgacatcgc cgtggagtgg gagagcaatg ggcagccgga gaacaactac aagaccacgc 1860
ctcccgtgct ggactccgac ggctccttct tcctctacag caagctcacc gtggacaaga 1920
gcaggtggca gcaggggaac gtcttctcat gctccgtgat gcatgaggct ctgcacaacc 1980
actacacgca gaagagcctc tccctgtctc ccggtaaatg a                     2021

<210> 54
<211> 472
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 54
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser

 1               5                   10                  15
Val Ile Ile Ser Arg Gly Glu Val Gln Leu Val Glu Ser Gly Gly Gly
            20                  25                  30
Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly
        35                  40                  45
Phe Asn Ile Lys Asp Thr Tyr Ile His Trp Val Arg Gln Ala Pro Gly
    50                  55                  60
Lys Gly Leu Glu Trp Val Ala Arg Ile Tyr Pro Thr Asn Gly Tyr Thr
65                  70                  75                  80
Arg Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Ala Asp Thr
                85                  90                  95
Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp
            100                 105                 110
Thr Ala Val Tyr Tyr Cys Ser Arg Trp Gly Gly Asp Gly Phe Tyr Ala
        115                 120                 125
Met Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser
    130                 135                 140
Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr
145                 150                 155                 160
Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro
                165                 170                 175
Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val
            180                 185                 190
His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser
        195                 200                 205
Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile
    210                 215                 220
Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val
225                 230                 235                 240
```

```
Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
                245                 250                 255
Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
            260                 265                 270
Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
        275                 280                 285
Val Asp Val Ser His Glu Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
    290                 295                 300
Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
305                 310                 315                 320
Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
                325                 330                 335
Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
            340                 345                 350
Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
        355                 360                 365
Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
    370                 375                 380
Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
385                 390                 395                 400
Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
                405                 410                 415
Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
            420                 425                 430
Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
        435                 440                 445
Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
    450                 455                 460
Ser Leu Ser Leu Ser Pro Gly Lys
465                 470
```

<210> 55
<211> 711
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 55

```
atggattttc aggtgcagat tttcagcttc ctgctaatca gtgcctcagt cataatatcc 60
agaggagaca tccagatgac ccagtccccg agctccctgt ccgcctctgt gggcgatagg 120
gttaccatca cctgccgtgc cagtcaggat gtgaatactg ctgtagcctg gtatcaacag 180
aaaccaggaa aagctccgaa actactgatt tactcggcat ccttcctcta ctctggagtc 240
ccttctcgct tctctggctc cagatctggg acggatttca ctctgaccat cagcagtctg 300
cagccggaag acttcgcaac ttattactgt cagcaacatt atactactcc tcccacgttc 360
ggacagggta ccaaggtgga gatcaaacgt actgtggctg caccatctgt cttcatcttc 420
ccgccatctg atgagcagtt gaaatctgga actgcctctg ttgtgtgcct gctgaataac 480
ttctatccca gagaggccaa agtacagtgg aaggtggata acgccctcca atcgggtaac 540
tcccaggaga gtgtcacaga gcaggacagc aaggacagca cctacagcct cagcagcacc 600
ctgacgctga gcaaagcaga ctacgagaaa cacaaagtct acgcctgcga agtcacccat 660
cagggcctga gctcgcccgt cacaaagagc ttcaacaggg gagagtgtta g          711
```

<210> 56
<211> 236
<212> PRT

<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 56
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
1   5   10   15
Val Ile Ile Ser Arg Gly Asp Ile Gln Met Thr Gln Ser Pro Ser Ser
            20   25   30
Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser
        35   40   45
Gln Asp Val Asn Thr Ala Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys
    50   55   60
Ala Pro Lys Leu Leu Ile Tyr Ser Ala Ser Phe Leu Tyr Ser Gly Val
65   70   75   80
Pro Ser Arg Phe Ser Gly Ser Arg Ser Gly Thr Asp Phe Thr Leu Thr
                85   90   95
Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln
            100   105   110
His Tyr Thr Thr Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
        115   120   125
Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
    130   135   140
Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
145   150   155   160
Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu
                165   170   175
Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp
            180   185   190
Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr
        195   200   205
Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser
    210   215   220
Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225   230   235

<210> 57
<211> 2489
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 57
atggattttc aggtgcagat tttcagcttc ctgctaatca gtgcctcagt cataatatcc 60
agaggagagg ttcagctggt ggagtctggc ggtggcctgg tgcagccagg gggctcactc 120
cgtttgtcct gtgcagcttc tggcttcaac attaaagaca cctatataca ctgggtgcgt 180
caggccccgg gtaagggcct ggaatgggtt gcaaggattt atcctacgaa tggttatact 240
agatatgccg atagcgtcaa gggccgtttc actataagcg cagacacatc caaaaacaca 300
gcctacctgc agatgaacag cctgcgtgct gaggacactg ccgtctatta ttgttctaga 360
tggggagggg acggcttcta tgctatggac tactggggtc aaggaaccct ggtcaccgtc 420
tcctcggcta gcaccaaggg cccatcggtc ttccccctgg caccctcctc caagagcacc 480
tctgggggca cagcggccct gggctgcctg gtcaaggact acttccccga accggtgacg 540

```
gtgtcttgga actcaggcgc cctgaccagc ggcgtgcaca ccttcccggc tgtcctacag 600
tcctcaggac tctactccct cagcagcgtg gtgaccgtgc cctccagcag cttgggcacc 660
cagacctaca tctgcaacgt gaatcacaag cccagcaaca ccaaggtgga caagaaagtt 720
ggtgagaggc cagcacaggg agggagggtg tctgctggaa gcaggctcag cgctcctgcc 780
tggacgcatc ccggctatgc agccccagtc cagggcagca aggcaggccc cgtctgcctc 840
ttcacccgga gcctctgccc gccccactca tgctcaggga gagggtcttc tggctttttc 900
ccaggctctg ggcaggcaca ggctaggtgc ccctaaccca ggccctgcac acaaaggggc 960
aggtgctggg ctcagacctg ccaagagcca tatccgggag gaccctgccc ctgacctaag 1020
cccaccccaa aggccaaact ctccactccc tcagctcgga caccttctct cctcccagat 1080
tccagtaact cccaatcttc tctctgcaga gcccaaatct tgtgacaaaa ctcacacatg 1140
cccaccgtgc ccaggtaagc cagcccaggc ctcgccctcc agctcaaggc gggacaggtg 1200
ccctagagta gcctgcatcc agggacaggc cccagccggg tgctgacacg tccacctcca 1260
tctcttcctc agcacctgaa ctcctggggg gaccgtcagt cttcctcttc cccccaaaac 1320
ccaaggacac cctcatgatc tcccggaccc ctgaggtcac atgcgtggtg gtggacgtga 1380
gccacgaaga ccctgaggtc aagttcaact ggtacgtgga cggcgtggag gtgcataatg 1440
ccaagacaaa gccgcgggag gagcagtaca acagcacgta ccgggtggtc tgcgtcctca 1500
ccgtcctgca ccaggactgg ctgaatggca aggagtacaa gtgcaaggtc tccaacaaag 1560
ccctcccagc ccccatcgag aaaaccatct ccaaagccaa aggtgggacc cgtggggtgc 1620
gagggccaca tggacagagg ccggctcggc ccaccctctg ccctgagagt gaccgctgta 1680
ccaacctctg tcctacaggg cagccccgag aaccacaggt gtacaccctg cccccatccc 1740
gggatgagct gaccaagaac caggtcagcc tgacctgcct ggtcaaaggc ttctatccca 1800
gcgacatcgc cgtggagtgg gagagcaatg ggcagccgga gaacaactac aagaccacgc 1860
ctcccgtgct ggactccgac ggctccttct tcctctacag caagctcacc gtggacaaga 1920
gcaggtggca gcaggggaac gtcttctcat gctccgtgat gcatgaggct ctgcacaacc 1980
actacacgca gaagagcctc tccctgtctc ccggtaaaac ccaggactgc tccttccaac 2040
acagccccat ctcctccgac ttcgctgtca aaatccgtga gctgtctgac tacctgcttc 2100
aagattaccc agtcaccgtg gcctccaacc tgcaggacga ggagctctgc gggggcctct 2160
ggcggctggt cctggcacag cgctggatgg agcggctcaa gactgtcgct gggtccaaga 2220
tgcaaggctt gctggagcgc gtgaacacgg agatacactt tgtcaccaaa tgtgcctttc 2280
agcccccccc cagctgtctt cgcttcgtcc agaccaacat ctcccgcctc ctgcaggaga 2340
cctccgagca gctggtggcg ctgaagccct ggatcactcg ccagaacttc tcccggtgcc 2400
tggagctgca gtgtcagccc gactcctcaa ccctgccacc cccatggagt ccccggcccc 2460
tggaggccac agccccgaca gccccgtga                                   2489

<210> 58
<211> 628
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 58
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1               5                  10                  15
Val Ile Ile Ser Arg Gly Glu Val Gln Leu Val Glu Ser Gly Gly Gly
            20                  25                  30
Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly
        35                  40                  45
Phe Asn Ile Lys Asp Thr Tyr Ile His Trp Val Arg Gln Ala Pro Gly
    50                  55                  60
Lys Gly Leu Glu Trp Val Ala Arg Ile Tyr Pro Thr Asn Gly Tyr Thr
65                  70                  75                  80
Arg Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Ala Asp Thr
                85                  90                  95
Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp
            100                 105                 110
```

```
Thr Ala Val Tyr Tyr Cys Ser Arg Trp Gly Gly Asp Gly Phe Tyr Ala
        115                 120                 125
Met Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser
    130                 135                 140
Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr
145                 150                 155                 160
Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro
                165                 170                 175
Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val
            180                 185                 190
His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser
        195                 200                 205
Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile
    210                 215                 220
Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val
225                 230                 235                 240
Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
                245                 250                 255
Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
            260                 265                 270
Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
        275                 280                 285
Val Asp Val Ser His Glu Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
    290                 295                 300
Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
305                 310                 315                 320
Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
                325                 330                 335
Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
            340                 345                 350
Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
        355                 360                 365
Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
    370                 375                 380
Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
385                 390                 395                 400

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
                405                 410                 415
Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
            420                 425                 430
Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
        435                 440                 445
Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
    450                 455                 460
Ser Leu Ser Leu Ser Pro Gly Lys Thr Gln Asp Cys Ser Phe Gln His
465                 470                 475                 480
Ser Pro Ile Ser Ser Asp Phe Ala Val Lys Ile Arg Glu Leu Ser Asp
                485                 490                 495
Tyr Leu Leu Gln Asp Tyr Pro Val Thr Val Ala Ser Asn Leu Gln Asp
            500                 505                 510
Glu Glu Leu Cys Gly Gly Leu Trp Arg Leu Val Leu Ala Gln Arg Trp
        515                 520                 525
Met Glu Arg Leu Lys Thr Val Ala Gly Ser Lys Met Gln Gly Leu Leu
    530                 535                 540
Glu Arg Val Asn Thr Glu Ile His Phe Val Thr Lys Cys Ala Phe Gln
545                 550                 555                 560
```

Pro Pro Pro Ser Cys Leu Arg Phe Val Gln Thr Asn Ile Ser Arg Leu
565 570 575
Leu Gln Glu Thr Ser Glu Gln Leu Val Ala Leu Lys Pro Trp Ile Thr
580 585 590
Arg Gln Asn Phe Ser Arg Cys Leu Glu Leu Gln Cys Gln Pro Asp Ser
595 600 605
Ser Thr Leu Pro Pro Pro Trp Ser Pro Arg Pro Leu Glu Ala Thr Ala
610 615 620
Pro Thr Ala Pro
625

<210> 59
<211> 2534
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 59
atggattttc aggtgcagat tttcagcttc ctgctaatca gtgcctcagt cataatatcc 60
agaggagagg ttcagctggt ggagtctggc ggtggcctgg tgcagccagg gggctcactc 120
cgtttgtcct gtgcagcttc tggcttcaac attaaagaca cctatataca ctgggtgcgt 180
caggccccgg gtaagggcct ggaatgggtt gcaaggattt atcctacgaa tggttatact 240
agatatgccg atagcgtcaa gggccgtttc actataagcg cagacacatc caaaaacaca 300
gcctacctgc agatgaacag cctgcgtgct gaggacactg ccgtctatta ttgttctaga 360
tggggagggg acggcttcta tgctatggac tactggggtc aaggaaccct ggtcaccgtc 420
tcctcggcta gcaccaaggg cccatcggtc ttccccctgg caccctcctc caagagcacc 480
tctgggggca cagcggccct gggctgcctg gtcaaggact acttccccga accggtgacg 540
gtgtcttgga actcaggcgc cctgaccagc ggcgtgcaca ccttcccggc tgtcctacag 600
tcctcaggac tctactccct cagcagcgtg gtgaccgtgc cctccagcag cttgggcacc 660
cagacctaca tctgcaacgt gaatcacaag cccagcaaca ccaaggtgga caagaaagtt 720
ggtgagaggc cagcacaggg agggagggtg tctgctggaa gcaggctcag cgctcctgcc 780
tggacgcatc ccggctatgc agccccagtc cagggcagca aggcaggccc cgtctgcctc 840
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ccaggctctg ggcaggcaca ggctaggtgc ccctaaccca ggccctgcac acaaaggggc 960
aggtgctggg ctcagacctg ccaagagcca tatccgggag gaccctgccc ctgacctaag 1020
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tccagtaact cccaatcttc tctctgcaga gcccaaatct tgtgacaaaa ctcacacatg 1140
cccaccgtgc ccaggtaagc cagcccaggc ctcgccctcc agctcaaggc gggacaggtg 1200
ccctagagta gcctgcatcc agggacaggc cccagccggg tgctgacacg tccacctcca 1260
tctcttcctc agcacctgaa ctcctggggg gaccgtcagt cttcctcttc cccccaaaac 1320
ccaaggacac cctcatgatc tcccggaccc ctgaggtcac atgcgtggtg gtggacgtga 1380
gccacgaaga ccctgaggtc aagttcaact ggtacgtgga cggcgtggag gtgcataatg 1440
ccaagacaaa gccgcgggag gagcagtaca acagcacgta ccgggtggtc tgcgtcctca 1500
ccgtcctgca ccaggactgg ctgaatggca aggagtacaa gtgcaaggtc tccaacaaag 1560
ccctcccagc ccccatcgag aaaaccatct ccaaagccaa aggtgggacc cgtggggtgc 1620
gagggccaca tggacagagg ccggctcggc ccaccctctg ccctgagagt gaccgctgta 1680
ccaacctctg tcctacaggg cagccccgag aaccacaggt gtacaccctg cccccatccc 1740
gggatgagct gaccaagaac caggtcagcc tgacctgcct ggtcaaaggc ttctatccca 1800
gcgacatcgc cgtggagtgg gagagcaatg ggcagccgga gaacaactac aagaccacgc 1860
ctcccgtgct ggactccgac ggctccttct tcctctacag caagctcacc gtggacaaga 1920
gcaggtggca gcaggggaac gtcttctcat gctccgtgat gcatgaggct ctgcacaacc 1980
actacacgca gaagagcctc tccctgtctc ccggtaaagg cggtggaggc tctggtggag 2040
gcggttcagg aggcggtgga tctacccagg actgctcctt ccaacacagc cccatctcct 2100
ccgacttcgc tgtcaaaatc cgtgagctgt ctgactacct gcttcaagat tacccagtca 2160

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ccgtggcctc caacctgcag gacgaggagc tctgcggggg cctctggcgg ctggtcctgg 2220
cacagcgctg gatggagcgg ctcaagactg tcgctgggtc caagatgcaa ggcttgctgg 2280
agcgcgtgaa cacggagata cactttgtca ccaaatgtgc ctttcagccc ccccccagct 2340
gtcttcgctt cgtccagacc aacatctccc gcctcctgca ggagacctcc gagcagctgg 2400
tggcgctgaa gccctggatc actcgccaga acttctcccg gtgcctggag ctgcagtgtc 2460
agcccgactc ctcaaccctg ccaccccccat ggagtccccg gcccctggag gccacagccc 2520
cgacagcccc gtga                                                   2534

<210> 60
<211> 643
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 60
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1               5                  10                  15
Val Ile Ile Ser Arg Gly Glu Val Gln Leu Val Glu Ser Gly Gly Gly
            20                  25                  30
Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly
        35                  40                  45
Phe Asn Ile Lys Asp Thr Tyr Ile His Trp Val Arg Gln Ala Pro Gly
    50                  55                  60
Lys Gly Leu Glu Trp Val Ala Arg Ile Tyr Pro Thr Asn Gly Tyr Thr
65                  70                  75                  80
Arg Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Ala Asp Thr
                85                  90                  95
Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp
            100                 105                 110
Thr Ala Val Tyr Tyr Cys Ser Arg Trp Gly Gly Asp Gly Phe Tyr Ala
        115                 120                 125
Met Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser
    130                 135                 140
Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr
145                 150                 155                 160
Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro
                165                 170                 175
Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val
            180                 185                 190
His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser
        195                 200                 205
Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile
    210                 215                 220
Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val
225                 230                 235                 240
Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
                245                 250                 255
Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
            260                 265                 270
Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
        275                 280                 285
Val Asp Val Ser His Glu Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
    290                 295                 300
Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
305                 310                 315                 320
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Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
325 330 335
Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
340 345 350
Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
355 360 365
Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
370 375 380
Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
385 390 395 400
Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
405 410 415
Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
420 425 430
Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
435 440 445
Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
450 455 460
Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly Gly
465 470 475 480
Gly Ser Gly Gly Gly Gly Ser Thr Gln Asp Cys Ser Phe Gln His Ser
485 490 495
Pro Ile Ser Ser Asp Phe Ala Val Lys Ile Arg Glu Leu Ser Asp Tyr
500 505 510
Leu Leu Gln Asp Tyr Pro Val Thr Val Ala Ser Asn Leu Gln Asp Glu
515 520 525
Glu Leu Cys Gly Gly Leu Trp Arg Leu Val Leu Ala Gln Arg Trp Met
530 535 540
Glu Arg Leu Lys Thr Val Ala Gly Ser Lys Met Gln Gly Leu Leu Glu
545 550 555 560
Arg Val Asn Thr Glu Ile His Phe Val Thr Lys Cys Ala Phe Gln Pro
565 570 575
Pro Pro Ser Cys Leu Arg Phe Val Gln Thr Asn Ile Ser Arg Leu Leu
580 585 590
Gln Glu Thr Ser Glu Gln Leu Val Ala Leu Lys Pro Trp Ile Thr Arg
595 600 605
Gln Asn Phe Ser Arg Cys Leu Glu Leu Gln Cys Gln Pro Asp Ser Ser
610 615 620
Thr Leu Pro Pro Pro Trp Ser Pro Arg Pro Leu Glu Ala Thr Ala Pro
625 630 635 640
Thr Ala Pro

<210> 61
<211> 1998
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 61
atgacagtgc tggcgccagc ctggagccca acaacctatc tcctcctgct gctgctgctg 60
agctcgggac tcagtgggac ccaggactgc tccttccaac acagccccat ctcctccgac 120
ttcgctgtca aaatccgtga gctgtctgac tacctgcttc aagattaccc agtcaccgtg 180
gcctccaacc tgcaggacga ggagctctgc gggggcctct ggcggctggt cctggcacag 240

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cgctggatgg agcggctcaa gactgtcgct gggtccaaga tgcaaggctt gctggagcgc 300
gtgaacacgg agatacactt tgtcaccaaa tgtgcctttc agcccccccc cagctgtctt 360
cgcttcgtcc agaccaacat ctcccgcctc ctgcaggaga cctccgagca gctggtggcg 420
ctgaagccct ggatcactcg ccagaacttc tcccggtgcc tggagctgca gtgtcagccc 480
gactcctcaa ccctgccacc cccatggagt ccccggcccc tggaggccac agccccgaca 540
gccccggagc ccaaatcttg tgacaaaact cacacatgcc caccgtgccc agcacctgaa 600
ctcctggggg gaccgtcagt cttcctcttc cccccaaaac ccaaggacac cctcatgatc 660
tcccggaccc ctgaggtcac atgcgtggtg gtggacgtga gccacgaaga ccctgaggtc 720
aagttcaact ggtacgtgga cggcgtggag gtgcataatg ccaagacaaa gccgcgggag 780
gagcagtaca acagcacgta ccgggtggtc tgcgtcctca ccgtcctgca ccaggactgg 840
ctgaatggca aggagtacaa gtgcaaggtc tccaacaaag ccctcccagc ccccatcgag 900
aaaaccatct ccaaagccaa agggcagccc cgagaaccac aggtgtacac cctgccccca 960
tcccgggatg agctgaccaa gaaccaggtc agcctgacct gcctggtcaa aggcttctat 1020
cccagcgaca tcgccgtgga gtgggagagc aatgggcagc cggagaacaa ctacaagacc 1080
acgcctcccg tgctggactc cgacggctcc ttcttcctct acagcaagct caccgtggac 1140
aagagcaggt ggcagcaggg gaacgtcttc tcatgctccg tgatgcatga ggctctgcac 1200
aaccactaca cgcagaagag cctctccctg tctcccggta aagaggttca gctggtggag 1260
tctggcggtg gcctggtgca gccagggggc tcactccgtt tgtcctgtgc agcttctggc 1320
ttcaacatta aagacaccta tatacactgg gtgcgtcagg ccccgggtaa gggcctggaa 1380
tgggttgcaa ggatttatcc tacgaatggt tatactagat atgccgatag cgtcaagggc 1440
cgtttcacta taagcgcaga cacatccaaa aacacagcct acctgcagat gaacagcctg 1500
cgtgctgagg acactgccgt ctattattgt tctagatggg gaggggacgg cttctatgct 1560
atggactact ggggtcaagg aaccctggtc accgtctcct cggctagcac caagggccca 1620
tcggtcggcg gtggaggctc tggtggaggc ggttcaggag gcggtggatc tgacatccag 1680
atgacccagt ccccgagctc cctgtccgcc tctgtgggcg atagggttac catcacctgc 1740
cgtgccagtc aggatgtgaa tactgctgta gcctggtatc aacagaaacc aggaaaagct 1800
ccgaaactac tgatttactc ggcatccttc ctctactctg gagtcccttc tcgcttctct 1860
ggctccagat ctgggacgga tttcactctg accatcagca gtctgcagcc ggaagacttc 1920
gcaacttatt actgtcagca acattatact actcctccca cgttcggaca gggtaccaag 1980
gtggagatca aacgttga                                                1998

<210> 62
<211> 665
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 62
Met Thr Val Leu Ala Pro Ala Trp Ser Pro Thr Thr Tyr Leu Leu Leu
 1               5                  10                  15
Leu Leu Leu Leu Ser Ser Gly Leu Ser Gly Thr Gln Asp Cys Ser Phe
            20                  25                  30
Gln His Ser Pro Ile Ser Ser Asp Phe Ala Val Lys Ile Arg Glu Leu
        35                  40                  45
Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val Thr Val Ala Ser Asn Leu
    50                  55                  60
Gln Asp Glu Glu Leu Cys Gly Gly Leu Trp Arg Leu Val Leu Ala Gln
65                  70                  75                  80
Arg Trp Met Glu Arg Leu Lys Thr Val Ala Gly Ser Lys Met Gln Gly
                85                  90                  95
Leu Leu Glu Arg Val Asn Thr Glu Ile His Phe Val Thr Lys Cys Ala
            100                 105                 110
Phe Gln Pro Pro Pro Ser Cys Leu Arg Phe Val Gln Thr Asn Ile Ser
        115                 120                 125
Arg Leu Leu Gln Glu Thr Ser Glu Gln Leu Val Ala Leu Lys Pro Trp
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    130                 135                 140
Ile Thr Arg Gln Asn Phe Ser Arg Cys Leu Glu Leu Gln Cys Gln Pro

145                 150                 155                 160
Asp Ser Ser Thr Leu Pro Pro Pro Trp Ser Pro Arg Pro Leu Glu Ala
                165                 170                 175
Thr Ala Pro Thr Ala Pro Glu Pro Lys Ser Cys Asp Lys Thr His Thr
            180                 185                 190
Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe
        195                 200                 205
Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
    210                 215                 220
Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
225                 230                 235                 240
Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
                245                 250                 255
Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
            260                 265                 270
Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
        275                 280                 285
Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
    290                 295                 300
Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
305                 310                 315                 320
Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
                325                 330                 335
Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
            340                 345                 350
Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
        355                 360                 365
Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
    370                 375                 380
Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
385                 390                 395                 400
Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Glu Val
                405                 410                 415
Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu
            420                 425                 430
Arg Leu Ser Cys Ala Ala Ser Gly Phe Asn Ile Lys Asp Thr Tyr Ile
        435                 440                 445
His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg
    450                 455                 460
Ile Tyr Pro Thr Asn Gly Tyr Thr Arg Tyr Ala Asp Ser Val Lys Gly
465                 470                 475                 480
Arg Phe Thr Ile Ser Ala Asp Thr Ser Lys Asn Thr Ala Tyr Leu Gln
                485                 490                 495
Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ser Arg
            500                 505                 510
Trp Gly Gly Asp Gly Phe Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr
        515                 520                 525
Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Gly Gly
    530                 535                 540
Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln
545                 550                 555                 560
Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val
                565                 570                 575
Thr Ile Thr Cys Arg Ala Ser Gln Asp Val Asn Thr Ala Val Ala Trp
```

580 585 590
Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ser Ala
595 600 605
Ser Phe Leu Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Arg Ser
610 615 620
Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe
625 630 635 640
Ala Thr Tyr Tyr Cys Gln Gln His Tyr Thr Thr Pro Pro Thr Phe Gly
645 650 655
Gln Gly Thr Lys Val Glu Ile Lys Arg
660 665

<210> 63
<211> 1098
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 63
atgacagtgc tggcgccagc ctggagccca acaacctatc tcctcctgct gctgctgctg 60
agctcgggac tcagtgggac ccaggactgc tccttccaac acagccccat ctcctccgac 120
ttcgctgtca aaatccgtga gctgtctgac tacctgcttc aagattaccc agtcaccgtg 180
gcctccaacc tgcaggacga ggagctctgc gggggcctct ggcggctggt cctggcacag 240
cgctggatgg agcggctcaa gactgtcgct gggtccaaga tgcaaggctt gctggagcgc 300
gtgaacacgg agatacactt tgtcaccaaa tgtgcctttc agcccccccc cagctgtctt 360
cgcttcgtcc agaccaacat ctcccgcctc ctgcaggaga cctccgagca gctggtggcg 420
ctgaagccct ggatcactcg ccagaacttc tcccggtgcc tggagctgca gtgtcagccc 480
gactcctcaa ccctgccacc cccatggagt ccccggcccc tggaggccac agccccgaca 540
gccccgggcg gtggaggctc tggtggaggc ggttcaggag gcggtggatc tgtgagagaa 600
agaggtcctc agagagtagc agctcacata actgggacca gaggaagaag caacacattg 660
tcttctccaa actccaagaa tgaaaaggct ctgggccgca aaataaactc ctgggaatca 720
tcaaggagtg ggcattcatt cctgagcaac ttgcacttga ggaatggtga actggtcatc 780
catgaaaaag ggttttacta catctattcc caaacatact ttcgatttca ggaggaaata 840
aaagaaaaca caaagaacga caaacaaatg gtccaatata tttacaaata cacaagttat 900
cctgacccta tattgttgat gaaaagtgct agaaatagtt gttggtctaa agatgcagaa 960
tatggactct attccatcta tcaaggggga atatttgagc ttaaggaaaa tgacagaatt 1020
tttgtttctg taacaaatga gcacttgata gacatggacc atgaagccag tttttttggg 1080
gcctttttag ttggctaa 1098

<210> 64
<211> 365
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 64
Met Thr Val Leu Ala Pro Ala Trp Ser Pro Thr Thr Tyr Leu Leu Leu
1 5 10 15
Leu Leu Leu Leu Ser Ser Gly Leu Ser Gly Thr Gln Asp Cys Ser Phe
20 25 30
Gln His Ser Pro Ile Ser Ser Asp Phe Ala Val Lys Ile Arg Glu Leu
35 40 45

```
Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val Thr Val Ala Ser Asn Leu
    50                  55                  60
Gln Asp Glu Glu Leu Cys Gly Gly Leu Trp Arg Leu Val Leu Ala Gln
65                  70                  75                  80
Arg Trp Met Glu Arg Leu Lys Thr Val Ala Gly Ser Lys Met Gln Gly
                85                  90                  95
Leu Leu Glu Arg Val Asn Thr Glu Ile His Phe Val Thr Lys Cys Ala
            100                 105                 110
Phe Gln Pro Pro Pro Ser Cys Leu Arg Phe Val Gln Thr Asn Ile Ser
        115                 120                 125
Arg Leu Leu Gln Glu Thr Ser Glu Gln Leu Val Ala Leu Lys Pro Trp
    130                 135                 140
Ile Thr Arg Gln Asn Phe Ser Arg Cys Leu Glu Leu Gln Cys Gln Pro
145                 150                 155                 160
Asp Ser Ser Thr Leu Pro Pro Pro Trp Ser Pro Arg Pro Leu Glu Ala
                165                 170                 175
Thr Ala Pro Thr Ala Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
            180                 185                 190
Gly Gly Gly Gly Ser Val Arg Glu Arg Gly Pro Gln Arg Val Ala Ala
        195                 200                 205
His Ile Thr Gly Thr Arg Gly Arg Ser Asn Thr Leu Ser Ser Pro Asn
    210                 215                 220
Ser Lys Asn Glu Lys Ala Leu Gly Arg Lys Ile Asn Ser Trp Glu Ser
225                 230                 235                 240
Ser Arg Ser Gly His Ser Phe Leu Ser Asn Leu His Leu Arg Asn Gly
                245                 250                 255
Glu Leu Val Ile His Glu Lys Gly Phe Tyr Tyr Ile Tyr Ser Gln Thr
            260                 265                 270
Tyr Phe Arg Phe Gln Glu Glu Ile Lys Glu Asn Thr Lys Asn Asp Lys
        275                 280                 285
Gln Met Val Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr Pro Asp Pro Ile
    290                 295                 300
Leu Leu Met Lys Ser Ala Arg Asn Ser Cys Trp Ser Lys Asp Ala Glu
305                 310                 315                 320
Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly Gly Ile Phe Glu Leu Lys Glu
                325                 330                 335
Asn Asp Arg Ile Phe Val Ser Val Thr Asn Glu His Leu Ile Asp Met
            340                 345                 350
Asp His Glu Ala Ser Phe Phe Gly Ala Phe Leu Val Gly
        355                 360                 365
```

<210> 65
<211> 1203
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 65

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atgacagtgc tggcgccagc ctggagccca acaacctatc tcctcctgct gctgctgctg 60
agctcgggac tcagtgggac ccaggactgc tccttccaac acagccccat ctcctccgac 120
ttcgctgtca aaatccgtga gctgtctgac tacctgcttc aagattaccc agtcaccgtg 180
gcctccaacc tgcaggacga ggagctctgc gggggcctct ggcggctggt cctggcacag 240
cgctggatgg agcggctcaa gactgtcgct gggtccaaga tgcaaggctt gctggagcgc 300
gtgaacacgg agatacactt tgtcaccaaa tgtgcctttc agcccccccc cagctgtctt 360
```

```
cgcttcgtcc agaccaacat ctcccgcctc ctgcaggaga cctccgagca gctggtggcg 420
ctgaagccct ggatcactcg ccagaacttc tcccggtgcc tggagctgca gtgtcagccc 480
gactcctcaa ccctgccacc cccatggagt ccccggcccc tggaggccac agccccgaca 540
gccccgatga agcagatcga ggacaaaatt gaggaaatcc tgtccaagat ttaccacatc 600
gagaacgaga tcgcccggat taagaaactc attggcgaga cctctgagga aaccatttct 660
acagttcaag aaaagcaaca aaatatttct cccctagtga gagaaagagg tcctcagaga 720
gtagcagctc acataactgg gaccagagga agaagcaaca cattgtcttc tccaaactcc 780
aagaatgaaa aggctctggg ccgcaaaata aactcctggg aatcatcaag gagtgggcat 840
tcattcctga gcaacttgca cttgaggaat ggtgaactgg tcatccatga aaaagggttt 900
tactacatct attcccaaac atactttcga tttcaggagg aaataaaaga aaacacaaag 960
aacgacaaac aaatggtcca atatatttac aaatacacaa gttatcctga ccctatattg 1020
ttgatgaaaa gtgctagaaa tagttgttgg tctaaagatg cagaatatgg actctattcc 1080
atctatcaag gggaatattt tgagcttaag gaaaatgaca gaatttttgt ttctgtaaca 1140
aatgagcact tgatagacat ggaccatgaa gccagttttt ttggggcctt tttagttggc 1200
taa                                                               1203

<210> 66
<211> 400
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 66
Met Thr Val Leu Ala Pro Ala Trp Ser Pro Thr Thr Tyr Leu Leu Leu
 1               5                   10                  15
Leu Leu Leu Leu Ser Ser Gly Leu Ser Gly Thr Gln Asp Cys Ser Phe
            20                  25                  30
Gln His Ser Pro Ile Ser Ser Asp Phe Ala Val Lys Ile Arg Glu Leu
        35                  40                  45
Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val Thr Val Ala Ser Asn Leu
    50                  55                  60
Gln Asp Glu Glu Leu Cys Gly Gly Leu Trp Arg Leu Val Leu Ala Gln
65                  70                  75                  80
Arg Trp Met Glu Arg Leu Lys Thr Val Ala Gly Ser Lys Met Gln Gly
                85                  90                  95
Leu Leu Glu Arg Val Asn Thr Glu Ile His Phe Val Thr Lys Cys Ala
            100                 105                 110
Phe Gln Pro Pro Pro Ser Cys Leu Arg Phe Val Gln Thr Asn Ile Ser
        115                 120                 125
Arg Leu Leu Gln Glu Thr Ser Glu Gln Leu Val Ala Leu Lys Pro Trp
    130                 135                 140
Ile Thr Arg Gln Asn Phe Ser Arg Cys Leu Glu Leu Gln Cys Gln Pro
145                 150                 155                 160
Asp Ser Ser Thr Leu Pro Pro Pro Trp Ser Pro Arg Pro Leu Glu Ala
                165                 170                 175
Thr Ala Pro Thr Ala Pro Met Lys Gln Ile Glu Asp Lys Ile Glu Glu
            180                 185                 190
Ile Leu Ser Lys Ile Tyr His Ile Glu Asn Glu Ile Ala Arg Ile Lys
        195                 200                 205
Lys Leu Ile Gly Glu Thr Ser Glu Glu Thr Ile Ser Thr Val Gln Glu
    210                 215                 220
Lys Gln Gln Asn Ile Ser Pro Leu Val Arg Glu Arg Gly Pro Gln Arg
225                 230                 235                 240
Val Ala Ala His Ile Thr Gly Thr Arg Gly Arg Ser Asn Thr Leu Ser
                245                 250                 255
```

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Ser Pro Asn Ser Lys Asn Glu Lys Ala Leu Gly Arg Lys Ile Asn Ser
            260                 265                 270
Trp Glu Ser Ser Arg Ser Gly His Ser Phe Leu Ser Asn Leu His Leu
        275                 280                 285
Arg Asn Gly Glu Leu Val Ile His Glu Lys Gly Phe Tyr Tyr Ile Tyr
    290                 295                 300
Ser Gln Thr Tyr Phe Arg Phe Gln Glu Glu Ile Lys Glu Asn Thr Lys
305                 310                 315                 320
Asn Asp Lys Gln Met Val Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr Pro
                325                 330                 335
Asp Pro Ile Leu Leu Met Lys Ser Ala Arg Asn Ser Cys Trp Ser Lys
            340                 345                 350
Asp Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly Gly Ile Phe Glu
        355                 360                 365
Leu Lys Glu Asn Asp Arg Ile Phe Val Ser Val Thr Asn Glu His Leu
    370                 375                 380
Ile Asp Met Asp His Glu Ala Ser Phe Phe Gly Ala Phe Leu Val Gly
385                 390                 395                 400
```

<210> 67
<211> 1749
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 67

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atgacagtgc tggcgccagc ctggagccca acaacctatc tcctcctgct gctgctgctg 60
agctcgggac tcagtgggac ccaggactgc tccttccaac acagccccat ctcctccgac 120
ttcgctgtca aaatccgtga gctgtctgac tacctgcttc aagattaccc agtcaccgtg 180
gcctccaacc tgcaggacga ggagctctgc gggggcctct ggcggctggt cctggcacag 240
cgctggatgg agcggctcaa gactgtcgct gggtccaaga tgcaaggctt gctggagcgc 300
gtgaacacgg agatacactt tgtcaccaaa tgtgcctttc agcccccccc cagctgtctt 360
cgcttcgtcc agaccaacat ctcccgcctc ctgcaggaga cctccgagca gctggtggcg 420
ctgaagccct ggatcactcg ccagaacttc tcccggtgcc tggagctgca gtgtcagccc 480
gactcctcaa ccctgccacc cccatggagt ccccggcccc tggaggccac agccccgaca 540
gccccggagc ccaaatcttg tgacaaaact cacacatgcc caccgtgccc agcacctgaa 600
ctcctggggg gaccgtcagt cttcctcttc cccccaaaac ccaaggacac cctcatgatc 660
tcccggaccc ctgaggtcac atgcgtggtg gtggacgtga gccacgaaga ccctgaggtc 720
aagttcaact ggtacgtgga cggcgtggag gtgcataatg ccaagacaaa gccgcgggag 780
gagcagtaca acagcacgta ccgggtggtc tgcgtcctca ccgtcctgca ccaggactgg 840
ctgaatggca aggagtacaa gtgcaaggtc tccaacaaag ccctcccagc ccccatcgag 900
aaaaccatct ccaaagccaa agggcagccc cgagaaccac aggtgtacac cctgccccca 960
tcccgggatg agctgaccaa gaaccaggtc agcctgacct gcctggtcaa aggcttctat 1020
cccagcgaca tcgccgtgga gtgggagagc aatgggcagc cggagaacaa ctacaagacc 1080
acgcctcccg tgctggactc cgacggctcc ttcttcctct acagcaagct caccgtggac 1140
aagagcaggt ggcagcaggg gaacgtcttc tcatgctccg tgatgcatga ggctctgcac 1200
aaccactaca cgcagaagag cctctccctg tctccggta aagtgagaga aagaggtcct 1260
cagagagtag cagctcacat aactgggacc agaggaagaa gcaacacatt gtcttctcca 1320
aactccaaga atgaaaaggc tctgggccgc aaaataaact cctgggaatc atcaaggagt 1380
gggcattcat tcctgagcaa cttgcacttg aggaatggtg aactggtcat ccatgaaaaa 1440
gggttttact acatctattc ccaaacatac tttcgatttc aggaggaaat aaaagaaaac 1500
acaaagaacg acaaacaaat ggtccaatat atttacaaat acacaagtta tcctgaccct 1560
atattgttga tgaaaagtgc tagaaatagt tgttggtcta aagatgcaga atatggactc 1620
```

```
tattccatct atcaaggggg aatatttgag cttaaggaaa atgacagaat ttttgtttct 1680
gtaacaaatg agcacttgat agacatggac catgaagcca gtttttttgg ggccttttta 1740
gttggctaa                                                         1749

<210> 68
<211> 582
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 68
Met Thr Val Leu Ala Pro Ala Trp Ser Pro Thr Thr Tyr Leu Leu Leu
 1               5                  10                  15
Leu Leu Leu Leu Ser Ser Gly Leu Ser Gly Thr Gln Asp Cys Ser Phe
            20                  25                  30
Gln His Ser Pro Ile Ser Ser Asp Phe Ala Val Lys Ile Arg Glu Leu
        35                  40                  45
Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val Thr Val Ala Ser Asn Leu
    50                  55                  60
Gln Asp Glu Glu Leu Cys Gly Gly Leu Trp Arg Leu Val Leu Ala Gln
65                  70                  75                  80
Arg Trp Met Glu Arg Leu Lys Thr Val Ala Gly Ser Lys Met Gln Gly
                85                  90                  95
Leu Leu Glu Arg Val Asn Thr Glu Ile His Phe Val Thr Lys Cys Ala
            100                 105                 110
Phe Gln Pro Pro Pro Ser Cys Leu Arg Phe Val Gln Thr Asn Ile Ser
        115                 120                 125
Arg Leu Leu Gln Glu Thr Ser Glu Gln Leu Val Ala Leu Lys Pro Trp
    130                 135                 140
Ile Thr Arg Gln Asn Phe Ser Arg Cys Leu Glu Leu Gln Cys Gln Pro
145                 150                 155                 160
Asp Ser Ser Thr Leu Pro Pro Pro Trp Ser Pro Arg Pro Leu Glu Ala
                165                 170                 175
Thr Ala Pro Thr Ala Pro Glu Pro Lys Ser Cys Asp Lys Thr His Thr
            180                 185                 190
Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe
        195                 200                 205
Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
    210                 215                 220
Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
225                 230                 235                 240
Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
                245                 250                 255
Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
            260                 265                 270
Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
        275                 280                 285
Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
    290                 295                 300
Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
305                 310                 315                 320
Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
                325                 330                 335
Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
            340                 345                 350
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Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
        355                 360                 365
Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
    370                 375                 380
Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
385                 390                 395                 400
Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Val Arg
                405                 410                 415
Glu Arg Gly Pro Gln Arg Val Ala Ala His Ile Thr Gly Thr Arg Gly
            420                 425                 430
Arg Ser Asn Thr Leu Ser Ser Pro Asn Ser Lys Asn Glu Lys Ala Leu
        435                 440                 445
Gly Arg Lys Ile Asn Ser Trp Glu Ser Ser Arg Ser Gly His Ser Phe
    450                 455                 460
Leu Ser Asn Leu His Leu Arg Asn Gly Glu Leu Val Ile His Glu Lys
465                 470                 475                 480
Gly Phe Tyr Tyr Ile Tyr Ser Gln Thr Tyr Phe Arg Phe Gln Glu Glu
                485                 490                 495
Ile Lys Glu Asn Thr Lys Asn Asp Lys Gln Met Val Gln Tyr Ile Tyr
            500                 505                 510
Lys Tyr Thr Ser Tyr Pro Asp Pro Ile Leu Leu Met Lys Ser Ala Arg
        515                 520                 525
Asn Ser Cys Trp Ser Lys Asp Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr
    530                 535                 540
Gln Gly Gly Ile Phe Glu Leu Lys Glu Asn Asp Arg Ile Phe Val Ser
545                 550                 555                 560
Val Thr Asn Glu His Leu Ile Asp Met Asp His Glu Ala Ser Phe Phe
                565                 570                 575
Gly Ala Phe Leu Val Gly
            580
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